

251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGGACA	TGACCGTGTG	CGATTTCCTC	ATCGGATGCA	TCGCGCACAC
351	TTTCAACCTC	AGCCTTAAAG	CGGATTTTCA	TGCGTGCCAA	AGGATGGTTG
401	CGGTCCACCA	CCGCTTTACC	TCGGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCCG	GTTTCAGGAT	CGTCGGCTTC	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GAACACGCCC	GCATCTTCAA	TACGGACCAA	CTCCGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGGCGAAAGC	GCCACATCGA	CCGSTATCGCC
601	GGCATCTCTT	CCTGCAACG	CCTCTTCCAC	CAAAGGGAAA	ATGCCGTCGT
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTTGTC	CAAAGCTGA
701	TTGTGGGCAT	CATACATCTC	ATAATGCAGC	GAACCACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTTTT	CAGGAACAGC	AGATTAAATA	CAGGCGCATT
801	CTAA				

```
a241.pep
1  MPTRPTRAAK HPTPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRRENHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHAQC RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDFNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTQORLFH QRENAVVTAV QIRNRFFGFV QKLIVGIHL IMORNHGILH
251 DSHICPFNRN RLITGAF*
```

```

                                10          20          30
m241.pep                      RQSVVVM TVRAVDM TVCDFLIGCIAHAFNC
                                |||||:|||||:|||||:|||||:|||||:
a241      QPTYLLHPSNKM PSEMEQ TLFRRHQIP PSCRQSVVVM TVRTVDM TVCDFLIGCIAHTFNR
                                70          80          90          100         110         120

                                40          50          60          70          80          90
m241.pep      SLKADFACQRMVAVHHRLAVGNIGYTIDDNIA GFRIVGFKHHADFD FNR EHARIFD TDQ
                                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      SLKADFACQRMVAVHHRLTVGNIGYTIDDNIA GFRIVGFKHHADFD FNR EHARIFN TDQ
                                130         140         150         160         170         180

                                100         110         120         130         140         150
m241.pep      LRILLAERIVGRQRHIDRIAGILT VQRLFHQRENA VVTAVQIRNRFFG FVQKLIVGI IHL
                                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      LRILLAERIVGRKRHIDRIAGILT VQRLFHQRENA VVTAVQIRNRFFG FVQKLIVGI IHL
                                190         200         210         220         230         240

                                160         170
m241.pep      IMQRNHGIFHDSHICPFNRN SRLITGAFX
                                |||||:|||||:|||||:|||||:|||||:
a241      IMQRNHGILHDSHICPFNRN SRLITGAFX
                                250         260

```

g241-1.seq

```
1 ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA ACGCGGTTT GCCCGCATCC AATGGCCTTG
201 CAATACAAAA CGTTTGTATT GTCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTTTGGGATC
301 GTAGCGGGGC GTATTGGCCA AGGCCAGGAT TTCCCCGGTG CGGGCATCCA
351 AACCACCCAC GATTCCGGCT TTGGCTGAT GGTATTCCAG CGCCTTGTTG
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGGCC GTTTTTCGGG CTCTTAKTGC CGGGGCGGCC AAGCTGTCCA
501 CAATATTGCC CTGCGCGTCC CGCAAAAGCA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTGCCCC ATCGGGTAAT
651 GCGGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTC AACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCGGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRA AK HPTPTWLQT AYCPRPYP RP SVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTWLQTAYCPRPYP RP SVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRA AKHPTPTWLQTAYCPRPYP RP SVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSN KMPSETEQTLFRRHQIPPS RQSVVMTVR AVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSN KMPSEMEQTLFRRHQIPPS RQSVVMTVR TVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFACQ RMVAVHRLAVGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIFD TDQ					
a241	SLKADFACQ RMVAVHRLTVGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIF NT DQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIV GRKRHDRIA GILTVQRLFHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL					
a241	LRILLAERIV GRKRHDRIA GILTVQRLFHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL					
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFH DSHICPFRNS RLITGAFX					
a241	IMQRNHGILH DSHICPFRNS RLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgctg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggatttcgc
201 tttcgtcgcg cacgccgccc aaggccatac ggacatatat ccgccccgtt
251 gctttggcga tggattcgcc caaagaggtt ttgccacgcg ccgaggggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggacgg
351 cgaggtatcc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcattccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgct gatgtagttg cgtacgacgg

```


557

	130	140	150	160	170	180
m242 . pep	QNPFDFDFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFQAVVVGIIHQSGFGDVFADAGFFLPRQSEQGVDDVAYDGGFGRHRHHHEFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLFDFICFQGIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDFACLGIIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVFEGFQLCQQEFHFPADFNGFNQLLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVFEGFQLCQQEFHFPADFNGFNQLLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

```

a242 . seq
1  ATGATCGGCG AACTTGTGTG TTTGCTCGGG ATCAAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCCCGG AAGTCGCTAN CCAATTGTG GATTTCGTGCG
101 AGCAGGAACA ATGGGTTTTT TACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATGGAGCCGA TATAGGTGCG GCGGTGTCCC CGGATTCGC
201 TTTCGTGCGC CACGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTGCGC CAAAGAGGTT TTGCCACGCG CTGGAGGGCC
301 GACCAGGCAC AGAATCGGCG CTTTGAGTTT GTCCATACGT TTTTGACGG
351 CGAGGTATTC CAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGCTCG
401 GTATCCAGCA CCAATCCGCG TTTGGCGATG TCTTTGCTGA CGCGGGATTT
451 TTTCTTCAC GGCAGTTCGA GCAGGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTGCGC AGACATCGGC GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGGCTTC TTTGGTCATA CCCGCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTCG TTCAGATAAT ATTCGCGCTG GGATTTTCC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATTT
801 CGGGAATTTC CAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAATGCG
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

```

a242 . pep
1  MIGELVVLG IKHFEQRAGG IAPEVAXQFV DFVEQEQWVF YAGFCHILQN
51  LTGHGADIGA AVSPDFAFVA HAAQSHADIF PPRCFGDGFA QRGFAHAWRA
101 DQAQNRAFEF VHTFLDGEVF QNPFDFDFQA VVVGIIHQSG FGDVFADAGF
151 FLPRQFEQGV DVVAYDGGFG RHRHHHFELF QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPADFNGFN QNLLALRQFQ LQMRCDRIG*

```

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLFIEHFEQRAGGIASEVVTQFVDFVEQEQGVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVVLGIIKHFEQRAGGIAPEVAXQFVDFVEQEQWVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFDFDFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					

559

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATJCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPM SFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVLPM SFLFSSTTGAVTKSX					
	:					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPM SFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagccccggc ggccgggttca gacggcattg ccgctttact
51  tcgatacggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatacgctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga ttgctgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttccac ggcaaaactc tgcctggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggccggcgcg cagggtttgc tcgtttgcc
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggtcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgctcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSGYYPSKIR
251 TFSRNFKQRQ EISHPPNTL PQPKYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCa GACGGCATTG CCGCTTTACT
51  TCGATCGGTTT TATACGCAAA AC GCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TFCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAATGCTT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAATTC TGTCGGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAACAAA TTGAAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFQLQVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFI GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFQLQVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFQLQVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFIHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFIHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRF TVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRF TVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

563

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

1	ATGCCGCTCTG	AAGCCCCGACA	GGCGGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGTT	TATACGCAAA	AGCGGCTTCA	GGAAATAAAT	CAGATTATTC
101	CCCAGACGCC	TTCAGGCTTC	CTTCTGTGCC	ACCGTAACCA	TAGCCGGGCG
151	CAACACGCGG	TCGGACAGCG	TACAAACCTT	CTTCATCAGC	CCCACCACGG
201	TATTGGGTTT	CTGTTCGGTT	GCCACGGCCT	GCATCGCGCT	ATGTGATATTC
251	GGATCGAGCT	TATCGCCCGC	TTTAGGATTG	ATTTCCTTGA	TTTGGGTAGC
301	ATCAAAATGCT	TTCTGCAACT	CGTTCAAAAT	CATCTGCAGC	CCCATTTTCA
351	GCGCATCGAA	ATTGCGCGCT	TGATCCAAAA	GGCGCAATTC	CAGATAATCC
401	TTGACCGGCA	GCATTTCAC	GGCAAACCTC	TGTCGGGGCA	ACTTGTGGGT
451	ATCCGCAATT	TCCTGCTGGT	TTCGCGCGCG	CAGGTTTTCG	TCGTTTGCCA
501	AAGCGCGCAG	CTGCTCGTCT	GGCAACTGCG	CTTCCAGCTC	GGCAATCCGC
551	GCCTGCAAA	CTCATAAAGC	CGGCTCTGCG	GCAGCCTGTT	CCTGCACACC
601	GTCGCGATT	CTCTACTGCT	CGACGGTTTC	CACCGCCTCC	ACATTTTCAA
651	CCGCTTCTTC	ACTGTTTTCG	TGCTGTGTCT	GTTCCGCTAT	ATCGTATCCC
701	TTAAAAACAA	TGGAAATCA	GAATCCAGTT	ATTACCCGCG	CAAGATAAGG
751	ACATTTTCAA	GGAACCTCAA	GCAAAGGCAG	AGAATTTCAA	ATTCAATTTT
801	AAATCCCTTA	CCGAAAAAAT	NA		

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

1	MPSEARQAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHHAHHGIGF	LFACHRLHRL	MDIRELIAR	FRIDFLDLSR
101	IKCFLQLVQS	HLHAHFQRIE	IAALIQKRHF	QIILDRQHFH	GKLLSGELVR
151	IRNFLVAAA	QVLLVCQSAQ	LVLFQLRFQL	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRLHIFNRF	TLVLLCLFAH	IVSLKTNWKS	KSSYYPKIR
251	TFSRNEFQQR	RISNSFNPL	PKK*		

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60	
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLRHNHNSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLCHRNHNSRAQHAVGQRITL					
	10	20	30	40	50	60	
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDF	LDLRSIKCFQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGIFLACHRLHRLMDIRIELIARFRIDF	LDLRSIKCFQLVQSHLHAHFQRIE					
	70	80	90	100	110	120	
m244-1.pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRI	RNFLLVAAQVLLVCQSA-LLVFQLRFQL					
a244-1	IAALIQKRHFQIILDRQHFHKGKLLSGELVRI	RNFLLVAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	179	
m244-1.pep	GNPRLQIILISRLCGSLFHTVRI	SYCLDGFHRLHIFNFFTVLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQIILISRLCGSLFHTVRI	SYCLDGFHRLHIFNFFTVLLCLFAHIVSLKTNWKS					
	180	190	200	210	220	230	239
m244-1.pep	GNPRLQIILISRLCGSLFHTVRI	SYCLDGFHRLHIFNFFTVLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQIILISRLCGSLFHTVRI	SYCLDGFHRLHIFNFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240	

565

	70	80	90	100	110	120
m246.pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	130	140	150	160		
	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1 ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCT
51 CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGCTGTA AATATCGGCG AGTGCTTTAC GGGCGAAGCC
151 GGTCACTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTACCTGCT CATTGGACG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1 MHGRNNGGTQA TVAFVFHQQT RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51 GOLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVVD FAGFGRFCRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQQT	RTCTCF	SNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR			
a246	MHGRNNGGTQATVAFVFHQQT	RTCTCF	SNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR			
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRNFACFKIMXQLDFLAD					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTC	HLDELAQVAFHRFNAFCFKIMVQLDFLAD				
	70	80	90	100	110	120
m246.pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	130	140	150	160		
	HRFAFDHQLAVFGCDDVVDFAFGFGRFCRPVYFYAQLGQVFFQLLQQ					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1 atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggatatgaa
51 ggggtttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gattttcgga atgcggcaac
201 attaatgtgc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaaagac gatattggtt attcaagtaa tcaaaactcaa
301 tctaaccctt gaaaaccccg tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattggata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgtc gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGGIDDLDAETAETVVSSCSKIAPGKKIST
130 140 150 160 170 180

m247.pep LEDAKKELKIPDQDKQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
|::||: |:| :|| | |||:|::| |||||::: ||||| ||||| |||||
g247 LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKWGNPQLL
190 200 210 220 230

g247 VKKVVRMDEVRYIYVSGCPEDDAGKEEFRTYNKFDSKNNAVTPAGVEVLDSGLNAKIA
240 250 260 270 280 290

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCTGTATGGC  GTGTCGATCG  AGTTATCTCA  CATCCCGGAA  ATTAATGAT
151 GCGGCAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTCGGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTCATAA
251 TGTCCGAGCA  TCTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  TACTAAAAAC  CGGTGCCAAA  CAAGAAAAATC  CCGTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCTATTGTC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGATGTTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAACAAA  ATGGAAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTTCGG  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCCG  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCTGTA  AAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCTGT  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCG  GGGGTGGAGG  TTPTATTGAG  TANCGGTACT
901 GATACCAAGA  TTCCGCCTTC  TTCAGACAA  CATATTATG  CTTACCGTAT
951 CGATCGGACA  ATACGCGGGG  GAAATGTATG  CGAAACAGA  CACTTTGA
```

a247.pep

1	MRRKMLNVPK	<u>GN</u> YDGMKGFT	<u>I</u> I EFLVAGML	SMIVLMAVGS	SYFTRSKLND
51	AANERLSAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHTKN	DIIVDSPKQT
101	QHPVPKPGAK	QENPLFSLEW	ANTNNTNNTT	AKLIPIAEST	DIKYPGFAQA
151	RPALIFQYGI	DDLDA S AE T V	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKKGKW	NPQLLVKKIR
251	HMKVRYIYVS	DCPEDDDAGK	EEKFYKTGTF	DSSTNAVPTA	GVEVLLSXGT
301	DTKIAASSDN	H1YAYRIDAT	IRGGNVCANR	TL*	

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTII	IEFLVAGLLSMIVLMAVGSSYFTSRKLNDAANERLAAQQ				
		:				:
a247	MRRKMLNVPKGNYDGMKGFTII	IEFLVAGMLSMIVLMAVGSSYFTSRKLNDAANERLSAQQ				
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI	-----	PDTTQQNSPFSLK-			
			: :	: :	:	
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDI	IIVDSPKQTOHVPVKPGAKQENPLFSLEW				
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK					
	:		: :	:		: :
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAETVVVSSCSKIAK					
	130	140	150	160	170	180

569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

              70      80      90      100      110      120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQNSPFS LKRNGIDK-LIPIAESSNI
              | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g247-1      PGAKQENPLFSLKRSMDKQLIPVAESIDI
              10      20      30

              130      140      150      160      170      180
m247-1.pep  NYQNFFQVGSALIFQYGI DDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
              | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g247-1      KYPGFIQRLNALVFQYGI DDLDASAETVVVSSCSKIAKPGKKISTLQEA KSA LQITNDDK
              40      50      60      70      80      90

              190      200      210      220      230      240
m247-1.pep  EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGK WGNPQLLVKKVRHMKVRYIYVS
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g247-1      -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGK WGNPQLLVKKVRHMDVRYIYVS
              100      110      120      130      140

              250      260      270      280      290      300
m247-1.pep  GCPEDDDAGKEETF KYTDKFD SAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g247-1      GCPEDDAGKEEFKRYTNKFD SKNAVTPAGVEVLLD SGLNAKIAASSD NSIYAYRINAT
              150      160      170      180      190      200

              310
m247-1.pep  IRGGNVCANRTLX
              | | | | | | | | | |
g247-1      IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTA AATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51 TCCGGGTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGCG AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTTCCG
401 ACTGTCTCTGA AGATGACGAT GCCGGCAAA AGGAAAAAAT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATATG TACCGTATC GATGCGACAA TACGCGGGG AAATGTATGC
601 GCAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial) ..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDL DASA ETVVSSCSK
51 IAKPGKKIST LQEA KSA LQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG K WGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEKFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNV
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | | | | | | | | | | | | | | | | | |
m247-1      GFGCFNMSEHPATDVIPDTTQNSPFS LKRNGIDKLIPIAESSNINYNQFFQVGSALIFQ
              80      90      100      110      120      130

              40      50      60      70      80      89
a247-1.pep  YGIDDL DASAETVVVSSCSKIAKPGKKISTLQEA KSA LQITNDDK-QNGNITRQRHVVN
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m247-1      YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVN
              140      150      160      170      180      190

              90      100      110      120      130      140      149
a247-1.pep  YAVGRIAGEEGLFRFQLDDKGK WGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEKFKY
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

571

```

g248      MRKQNTLTGIP TSDGQRGSALFIVLMVMIVVAVFLVVTAAQSYNTEQRISANESDRKLALS
           10          20          30          40          50          60

           50          60          70          80          90          100
m248.pep  LAEXXXREGELQVLDLEYPDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :||||||| : |||||||
g248      LAEAAALREGEFQVLDLEAADS KVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70          80          90          100          110          120

           110          120          130          140          150
m248.pep  TVEAVKRSCPA-----NSTDLCIDKKGXKEYKKGTRSVTKMPRYII EYLG VXNGENVYRVTA
           :||||||| |||||:| |||:| :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLG VKNGQNVYRVTA
           130          140          150          160          170          180

           160          170          180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           ||||||||| |||:|
g248      KAWGKNANTVVVLQSYVGNDEQX
           190          200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```
a248.seq
1  ATGCGCAAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA TCGTTTATCG TGCTGATGGT GATGATCGTG GTGGCTTTTT
101 TGGTTTGTAAC TGCCCGCGCAG TCCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAAACGTG GGAAAAGGTC TGTGTACCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAGAG
351 CAAGCCCAAC GTTGAGCGCG TGAGCGCTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAAG
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA
```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

a248.pep

1	MRKQNTLTGI	PTSDGQRGFA	<u>LFIVLMVMIV</u>	VAEFLVVTAAQ	SYNTEQRISA
51	NESDRKLALS	LAAEALREGE	LQVLDLEYDT	DSKVTFSENC	GKGLCTAVNV
101	RTNNDNEEAF	DNIVVQCKPT	VEAVKRSCTA	KSTGLCIDNK	GMEYKKGTPS
151	VSKMPRIYIE	YLGVKNGENV	YRVTAKAWGK	NANTVVVLQS	YVSNND*

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      10          20          30          40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248          MRKQNTLTGIIPTSDGQRGFALFIVLMMIVVAFLVVTAQSYNTEQRISANESDRKLALS
              10          20          30          40          50          60

              50          60          70          80          90          100
m248.pep      LAEXXXREGELQVLDDLEYDTSKVTFSENCCKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
              ||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
a248          LAEAALREGELQVLDDLEYDTSKVTFSENCCKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
              70          80          90          100          110          120

              110         120         130         140         150         160
m248.pep      VEAVKRSCPANSTDLCIDKKGXKEYKKGTGRSVTKMPRYIIIEYLGVMNGENVYRVTAKEWGW
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248          VEAVKRSCSTAKSTGLCIDNKGMEYKKGTQSVMKMPRYIIIEYLVKNGENVYRVTAKEWGW
              130         140         150         160         170         180

              170         180
m248.pep      NANTVVVLQSYVSNNDEX

```



```
g249.seq
1  atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51  gttgatgaga gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgtctgc cgtacagttg ccagcagctg cttccgtcag gagggcggaa
151 acgcaaacca tcgacagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accatcgatt tggacagcaa caagaaaaac tatagctctt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagattttg
351 tcatgagctg aaaaatgcct tgcgggatgc ggtagctatt cattaccccg
401 tctgcaagga ttctgcgggt gacgcgccga cattgtccga cagcgggtgt
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta cgtgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtga gcgcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga
```

g249.pap

1	MKNNDCLRLK	NPQSGMALIE	<u>VLVAMLVLT</u> I	<u>GILALLSVQ</u> L	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDLSNKKK	YSLYMGKQTL	SAVDGEFMLD
101	AEKSKAQLAE	EQLKRFSEL	KNALPDAVAI	HYAVCKDSSG	DAPTLSDSGA
151	FSSNCDNKAN	GDTLIKVLWV	NDSAGSDIS	RTNLEVSGDN	IVYTYQARVG
201	GRN*				

```
m249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  GATTCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGTGT  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101 CACTATTGTC  TGTACAGTTG  CGGACATCN  NNNNNNNNNN  NNNNNNNNNN
151 NNNNNNNNNN  NNNNNNNNNN  NNNNNNNNNN  NNNTTGATGG  AGGGAATGTT
201 GATGAATCCG  ACCATTGATT  CGGACAGCAA  CAAGAAAAAC  TATAATCTTT
251 ACATGGGAAA  CCATACACTA  TCAGCTGTGG  ATGGCGATT  TGGCATGTAG
301 GCCATGAAAA  CTAAGGGGCA  ATTGGCAGAG  GCACAATTGA  AGAGATTTAG
351 TTTAGAGCTG  AAAAAATGCC  TGCCCGATGC  GGCAGCCATC  CATTACGCCG
401 TCTGCAAGGA  TTCGTCGGGT  AACGCGCCGA  CATTGTCCGG  CAATGCTTTT
451 TCTTCAAATT  GCGACAATAA  GGCAACGGG  GATACTTTAA  TTAAAGTATT
501 GTGGGTAAAT  GATTCCGCAG  GGGATTCCGA  TATTTCCCGT  ACGAATCTTG
551 AGGTGAGCGG  CGACAATATC  GTATATACTT  ATCAGGCAAG  GGTCCGAGGT
601 CGGGAATGA
```

```
m249.pep
  1  MKNND CFLK  DSQSGMALIE  VLVAMLV LTI  GILALLSVQL  RTVXXXXXXXX
 51  XXXXXXXXXXX  XLM EGM LMNP  TIDSDSNKKN  YNL YMG NHTL  SAVDGDFAID
101 AMKTGQLAE  AQLKRFSYEL  KNALPDAAAI  HYAVCKDSSG  NAPTLSGNAF
151 SSNCDNKANG  DTLIKVLWVN  DSAGSDSISR  TNLEVS GDN I  VYTYQARVGG
201  RN*
```

m249.pep MKQND¹⁰CFR²⁰LKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXXX
| | | | : | | : | | | | | | | | | | | | | | | | | | | : : :

```

      180          190          200
m249.pep    SRTNLEVSGDNIIVYTYQARVGGREX
             :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
a249         ARTNLETNGNNIIVYTYQARVGGREX
              190          200

```

m249-1.seq

m249-1.pgp

m249-1/g249 90.1% identity in 203 aa overlap

m249-1.pep	10	20	30	40	50	60
	MKNND	CFRLK	DSQSG	MA	LIEV	LVA
g249	MKNND	CLRLK	NPQSG	MA	LIEV	LVA
m249-1.pep	70	80	90	100	110	120
	NLM	EGML	MNPT	ID	SD	SN
g249	NLM	EGML	MNPT	ID	SD	SN
m249-1.pep	130	140	150	160	170	179
	KNAL	PDA	AAI	HY	AV	CK
g249	KNAL	PDA	VAI	HY	AV	CK

```

      180      190      200
m249-1.pep  RTNLEVSGDNIIVYTYQARVGGREX
              |||||
g249         RTNLEVSGDNIIVYTYQARVGGREX
              190      200

```

a249/ L36117

```

>gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas
aeruginosa]
>gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader
sequence [Pseudomonas aeruginosa]
>gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
Score = 50.4 bits (118), Expect = 9e-06
Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

```

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQNLMEGMLMNPIT 72
QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIAQMGKTIQYTADSVERNKAAMLGSNLLESMRASPKA 71

Query: 73 DSDSNKKNNLYMGNNHHALSVDVGDGFQVDAIKTKTQLAEA---QLKRFSEYELKNALPDAA 129

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      59
m250.pep      MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
              |||:::|||||||||||||||||||||||:|||||:|||||
g250           MHTTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNPFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep      ATVNLWAEPLPILLIATVTFMINSRHI LMGGGACAPAPERNTAEKSRARTVFYVX
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g250           ATVNLWAEPLPILLIATITFMINSRHI LMGGGACHAHERNTAEKSRARAVFYV
              70      80      90      100     110

```

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGTG	ACAAAAGGC	ATGAGCTGCG	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGC	CTCCGAGTTT	GCCACGGCTA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTGC	TTATCGCCAC	CGTAAGCTTT	ATGATTAATT
251	CTCCGCATAT	CTGATGGGG	G.CGGCACTT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

```

1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMOGGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNWLAEPL PILLIATVTF MINSRHILMG XGTCPAPERN
101 TAEKSARTV FYV*

```

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLMTSMNFAGGSEF
      |
||:|||||||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLMTGMNFAGGSEF
          10          20          30          40          50
60
m250.pep          60          70          80          90          100          110
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRTVFYVX
|||||||||||||||||||||||||||||||||:|||||||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCAPAPERNTAEKSRTVFYVX
          70          80          90          100          110

```

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggaggctg gaacccaaac ggctcgtaac

```

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	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAIQVIGKRLV					
g251	MLIIIIILMAEVGTTKTVVTEVDAQVVADFGGIEGFFECRLQEPVAFPNHAIQVIGKRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRVRLKMIQTALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
g251	GTRAAIFVRTVGGTVRLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRHQRTVFAVGKQSAVFFVARVFAVTGQTRLFFICIKNRLGQECRNRIAR					
g251	VKHARTVFRHLRTVFTVGNQPAVFAAARVFAVASYRS-VFFIFIKNRLGQECRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```
a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCCACC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTGTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCCAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTGTGAAT GCCGCCTGCA AGAGCCTGTG GCTTTCGCCG
401 TAAATCACGC GGTGCGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGGCG GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCGTAGCG
601 GCTTTTGGTG TCGCTCTCGT CGTAAACAC GCCCGTACCG TATTCCGCGC
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCGCGCT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCGTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851 TTTTCAAAAC GAAAACCCGG GCGGAACAGC CACGATCGGC TTTCGTATGA
```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```
a251.pep
1  MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI IIILMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECRLQEPV AAFPVHAVGF VVGKRLVGTR
151 AAIFVRTVGR TVRLKMIQV TDALPVVREA GIIHPSVFIG IGIDIFQTV
201 AFGVRLVVKH ARTVFRHQRT TVFAVGKQTA VEVVARVFAV ASYRSVFSTF
251 IKNRLGQECR NRHIARVESL LRVFEYAADV VPFVFKTKTR AEQPRSAFV*
```

m251/a251 88.5% identity in 304 aa overlap

```
m251.pep      10      20      30      40      50      60
MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
a251          10      20      30      40      50      60
MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY

m251.pep      70      80      90     100     110     120
GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG
:||||  ::|||  |   |||  |||||||  |||||||  |||  |||||||
```

```
m253.seq
1  ATGATTGACA  GGAACCGTAT  GCTGCGGGAG  ACGTTGGAAC  GTGTGCGTGC
51  GGGGTGCTTC  TGGTTGTGTT  TGTGTGGCGC  GACGTTTGCA  TTTTTTACCG
101 GTTTTTCAGT  CAGTTATCTT  TGAATGGACA  ATCAGGGTCT  GAAATTTCTT
151 TTGGTTTTGG  CGGGCGTGTT  GGGCATGAAT  ACGCTGATGC  TGGCAGTATG
201 GTTGGAATG  TTGTTCTCTG  GTGTGAAAGT  GGGGCGTTTT  TTCAGCAGTC
251 CGGCGACGTG  GTTTCGGGGC  AAAGACCCCTG  TAAATCAGGC  GGTGTTGCGG
301 CTGTATGCGG  ACGGATGGCG  GCAACCTTCG  GTACGTTTGA  AAATAGGCGC
351 AACCTCGCAC  AGCCTGTGGC  CTGTGCACCT  GCTCGGAATG  CTGGTGTCTG
401 TATTGTTGCT  GCTTTTGGTG  CGGCAATATA  CGTTCAACTG  GGAAGGCACG
451 CTGTTGAGCA  ATGCCGCTTC  GGTACGCGCG  GTGGAATGT  TGGCATGGCT
501 GCCGTCGAAA  CTCGGTTTCC  CTGTCCCCGA  TGC CGGGCG  GTCATCGAAG
551 GCCGTCTGAA  CGGCAATATT  CGGCATGCGC  GGGCTTGGTC  GGGGCTGCTG
601 CTGGCGAGTA  TCGCTTGCTA  GCGGATCTGT  CCGCGCTCTG  TGCGTTGGGT
651 AGTGGTGAAA  ATCCTTTTGA  AAACAAGCGA  AAACGGATTG  GATTTGGAAA
701 AGCCCTATTA  TCAGGCGGTC  ATCCGCCGCT  GGCAGACAA  AATCACCGAT
751 GCGGATACGC  GTCGGGAAAC  CGTGTCGCCC  GTTTCACCGA  AAATCATCTT
801 GAACGATGCG  CCGAAATGGG  CGGTTCATGT  GGAGACCGAG  TGGCAGGACG
851 CGGAATGGTT  CGAGGGCAGG  CTGGCGCAGT  AATGGCTTGA  TAAGGCGCTT
901 GCCACCAATC  GGGAACAGGT  TGCCGCGCTG  GAGACAGAGC  TGAAGCAGAA
951 ACCGGCGCAA  CTGCTTATCG  GCGTGCGCGC  CCAAACGTG  CCGGACCGCG
1001 GCGTGTTGCG  GCAGATTGTC  CGACTCTCGG  AAGCGGCGCA  GGGCGGCGCG
1051 GTGGTGACAG  TTTTGGCGGA  ACAGGGGCTT  TCAGACGACC  TTTTCGAAAA
1101 GCTGTGAACG  TGGCGTAAAC  CGCTGGCCGA  ATGCGGCGCG  GCGTGGCTTG
1151 AGCCTGACAG  GGC CGGCAG  GAAGGCGCTT  TGAAAGACCA  ATAA
```

```
m253.pep
1  MIDRNRMLRE  TLERVRAGSF  WLWVVAATFA  FFTGFSVTYL  LMDNQGLNFF
51  LVLAGVLGMN  TLMLAVWLAM  LFLRLVKVGRF  FSSPATWFRG  KDPVNGQAVL
101  LVYADEWRQPS  VRWKIGATSH  SLWLCTLLGM  LVSVLLLLLV  RQYTFNWEST
151  LLSNAASVRA  VEMLAWLPSK  LGFPVPDARA  VIEGRNLNGNI  ADARAWSGLL
201  VGSIACYGIL  PRLLAHVVCK  ILLKTSSENGL  DLEKPPYQAV  IRRWQNKITD
251  ADTRRETVSA  VSPKIIILNDA  PKWAVMLETE  WQDGEWFEGR  LAQEWLDKGV
301  ATNREQVAAL  ETELKQKPAQ  LLIGVRAQTV  PDRGVLROQIV  RLSEAAQAGV
351  VQQLAEQGL  SDDLSEKLEH  WRNALAECGA  AWLEPDRAAQ  EGRLKDQ*
```

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGSVTYLLMDNQGLNFFLVLAGVLGMN					
	: :					
g253	MIDDRMLRDRTLERVAGSFWLWVVVASMMFTAGFSGTLYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSLLLLLVROYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLWLCTLLGMLVSLLLLLVROYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

583

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLEVRAGSFWLVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
m253.pep	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	VIEGRINGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRINGNIADARAWSGLLVGSIACYGILP.LLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	VIEGRINGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRINGNIADARAWSGLLVGSIACYGILP.LLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	IRRWQNKITDADTRRETSAVSPKII.LNDAPKWAVMLETEWQDGEWFEGLRAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIV.LNDAPKWAVMLETEWQDGEWFEGLRAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKII.LNDAPKWAVMLETEWQDGEWFEGLRAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIV.LNDAPKWAVMLETEWQDGEWFEGLRAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTV.PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTV.PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTV.PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTV.PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGLKDKQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGLKTDNRTX					
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGLKDKQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGLKTDNRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggcccggc
301 tggacgggat ttctactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggaacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cggcggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtatttg gcggcagcat aaccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDCRIF SVSVYGISLL

```

585

```

301 TGGACGGTAT TTCTACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CCGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTTACT GGTTTGTAAG CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254.pep

```

1 MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSIL
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

					10		20
30							
m254.pep							
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL							
a254							
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL							
		20	30	40	50		60
70							
		40	50	60	70		80
90							
m254.pep							
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS							
a254							
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS							
		80	90	100	110		120
130							
		100	110	120	130		140
150							
m254.pep							
IVIYVVMGWMVLAVMKSILTASLPSAGLAWLAAGGMLYSVGIIYWFVNDEKIRHGHGIWHLF							
a254							
IAIYIVMGWMVLAVMKSILTASLPPAGLAWLAAGGMLYSVGIIYWFVNDEKIRHGHGIWHLF							
		140	150	160	170		180
190							
		160					
m254.pep		VLGGSITQFVSVYGYVIX					
a254		VLGGSITQFVSVYGYVIX					
		200					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

130 140 150 160 170 180

	189
m255.pep	AALVGIADX
	:
g255	AALVGVADX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```
a255.seq
1 GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGTGC
51 CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGGTTGATG CCATCATGGC GTAGGCGATT TCGCATCGA GCGGGTCGAA
151 TACGGGTTGCG CCCAGCCGA CGGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCGCGAC GGAATCCAAG GATTTCGCGA CGCTGTCCAT ATAGTTTTCC
251 AGCTCGGCCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTGCGAC CTTCAAAACC GGATTTCTTT TTCGCGGACT TGGTGAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTTCTT TCAACCATTT TTTGGCAACG
401 GCTCCGCGCG CAACGCGGGC GCGGTTTTCG CGGCGGAAC TCCTGCGGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GCGCCGGGCG GAGCGGTGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

a255.pep

1	VVGQ	EALRGE	FVAV	FAAALR	YAVK	TCADFH	AFDG	VDAHHG	VGDF	GIEAVE
51	YGA	FQAQ	DGDV	GGFN	MQLRAD	GIQG	FAHAVH	IVFQ	LGNL	M
101	YFAA	FKPDDF	FADL	GNVGGD	FRAE	FFQPF	FGNG	SGGNAG	GGF	AGGT
151	APVV	ARAVFV	PIGI	VG	VAGA	EAGD	VA	VVF	AALV	GIAD*

m255/a255 93.1% identity in 188 aa overlap

		10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHA	FDGVD	DAHHR	VGD	FGIEAV	KNRFAQ	ADRD
a255	VVGQEALRGGEFVAVFAAALRYAVKTCADFHA	FDGVD	DAH	HGVGD	FGIEAV	EYGF	AQADGD
		10	20	30	40	50	60
		70	80	90	100	110	120
m255.pep	GC	FDMQL	RADGI	QGFA	HAVH	IVFQL	GNL
a255	GG	FNMQ	L	ADGI	QGFA	HAVH	IVFQL
		70	80	90	100	110	120
		130	140	150	160	170	180
m255.pep	FRA	EEFFQ	PFFG	NGSG	SNAGG	GTGG	APAAA
a255	FRA	EEFFQ	PFFG	NGSG	GNAGG	G	AGGT
		130	140	150	160	170	180
		189					
m255.pep	AAL	VGI	AD	X			
a255	AAL	VGI	AD	X			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```
g256.seq
1   atgctcgcgg  tacgcaatcg  ggggtggcac  ggcgcagtcg  tccatttccg
51  acagtcgcggc  ggcgtagcga  acacgcgcgc  ggtgttctac  cacttggggt
101 atatcgcgcga  aatcgccctt  gcttggaca  cgctcacccg  cgcgttaccg
151 gaaatatacg  ccgtcggcgt  atcgctgggc  ggcaacgcgc  cggcaaaaata
201 ttggggcgaa  cagggcaaaa  aggcattgcc  gcacgcctcg  gccgcgcgat
251 ccgcccccg  tgatgcagag  gcggcaggca  gcgcgttcga  cagcgccgat
301 acgcggctgc  tctacacgcg  ctacttcctc  cgcacactga  tccccaatg
```


589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```
a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGGTAGTCG TCCATTTCCG
51  CAGTGC GGCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCCTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGGCAGCA CCGCGGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```
a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPV FY HLGDTAEIAF TLDTLAARYR
51  EYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVGSTGGRLHL QWLPQTVLSY FDSFRTNRR*
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYX LGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWN GVVVHFRSCGGVANTAPVFYH LGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAE AAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAE AAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC KPLLKHVAKP LLLNNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC KPLLKHVAKP LLLNNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVG FVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```
g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACA CCGCGCACCC GCATACCGCC
```

591

```

g256-1      |||||
            LVVLFHGLEGSSRSHYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
            70      80      90      100     110     120

m256-1.pep  120      130      140      150      160      170      179
            TLDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRFRDSGI
            :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      ALDRTLARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGSRFRDSGI
            130      140      150      160      170      180

m256-1.pep  180      190      200      210      220      230      239
            TRLLYTRYFLRTLIPKAKSLQGFOTAFAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      TRLLYTRYFLRTLIPKARSLQGFOTAFAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSC
            190      200      210      220      230      240

m256-1.pep  240      250      260      270      280      290      299
            KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHL
            250      260      270      280      290      300

m256-1.pep  300      310      319
            QWLPQTVLSYFDSFRTNRRX
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      QWLPQTVLSYFDSFRTNRRX
            310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

a256-1.seq

```

1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACG CTCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCGTG GTCGTGCTGT TTCACGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGCGGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGGCAAAACG CGCTGCCGCA AGCCGCGGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCA ACACGATAC CCAAAGCACG GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGTCTA ATGCCGTCAG CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCAG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCTT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

a256-1.pep

```

1  MILTPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVFHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFA DR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHVG FV GSTGGRHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

a256-1.pep  10      20      30      40      50      60
            MILTPDTPFFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m256-1      MILTPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
            10      20      30      40      50      60

a256-1.pep  70      80      90      100     110     120
            VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVFHFRSCGGVANTAPVFYHLGDTAEIAFT
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m256-1      VVLFHGLEGSSRSHYAVELMLAVDRGWNGVVVFHFRSCGGIANTAPVFYHLGDTAEIAFT

```

593

```

m257.pep  MGRHFGRRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALLGSGAD
          |||||:||||:||||: |||||:||||| |||||:||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALLGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTCGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51  GCGGCGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAACT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVALLGSGAE  LRLFGVDDRR  AADLVNKVLA  EVARLEKMF  LYREDSLISE
101  LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFRTVAAVAAGXAASFLPNPFAADDEKRNKDEKRNENVFFWKGVALLGSGAX
          |||||      :|||||: |||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAGAAVSLPNPFAADDEKRNKDEKRNENVFFWKGVALLGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      LRLFGVDDRRRAADLVNKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GAAGCCGCGT
1451 GGGGCGAaGT GGCgaAgCG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGstGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCG CAATTATGCG
1651 CGTTCCCTT CGTCAAATT GGAAAATCAG GATTGAAAC CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPLVRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSL L AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

```

m258/g258

      10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLSAVLARYVILLK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAM L VLSAVLARYVILLK
      10      20      30      40      50      60

      70      80      90      100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL
      70      80      90      100     110     120

      130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SKSALDLAADNAVSNAVPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
      130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SINPHQFDQPLPDKEHWEQIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
      190     200     210     220     230     240

```

597

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVL SAV
51  LARYVILLK  DRRDGVFGSQ  IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAGGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLEDEQ DAQILTRSTD TI IKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVL SAV	LARYVILLK		
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVL SAV	LARYVILLK		
	10	20	30	40	50	60
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFING	TINSWFGNDTHEALERSLNL				
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHYAGSGFAQLAL	YNAASGKIEK			
a258	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHYAGSGFAQLAL	YNAASGKIEK			
	130	140	150	160	170	180
m258.pep	SINPHKLDQPFPGKARWEKI	QRAGSVRDLESIGGVLYAQQWLS	SAGTHNGRDYALFFRQPV			
a258	SINPHKLDQPFPGKARWEKI	QRAGSVRDLESIGGVLYAQQWLS	SAGTHNGRDYALFFRQPV			
	190	200	210	220	230	240
m258.pep	SINPHKLDQPFPGKARWEKI	QRAGSVRDLESIGGVLYAQQWLS	SAGTHNGRDYALFFRQPV			
a258	SINPHKLDQPFPGKARWEKI	QRAGSVRDLESIGGVLYAQQWLS	SAGTHNGRDYALFFRQPV			
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKKGLQTFFLATLLIAS	LLSIFLALVMALYFARRFVE			
a258	PKGVAEDAVLIEKARAKYAE	LSYSKKGLQTFFLATLLIAS	LLSIFLALVMALYFARRFVE			
	250	260	270	280	290	300
m258.pep	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEADERNRRREEAA			
a258	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEADERNRRREEAA			
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEADERNRRREEAA			
a258	PVLSLAEGAKAVAQGDFSQ	TRPVLRNDEFGRLTKLFNHMT	EQLSIAKEADERNRRREEAA			
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKAAEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL		
a258	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKAAEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL		
	370	380	390	400	410	420
m258.pep	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKILLGKATVLPED	NGNGVVMVIDDITVLIHAQK			
a258	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKILLGKATVLPED	NGNGVVMVIDDITVLIHAQK			

599

151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETI GRVFADIFELSALEGRAFGLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGR TQSGVAGDF KNIR					
g259	AEYKXHLRRC LPFGNGVGVGR AQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1 ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51 TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGCTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCGC
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCG GAAAAGTCCA
651 A

```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

```

1 MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51 ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG
201 RAQSGVAGDF KNIGKVQ

```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYT L L PPLLSALSAVALVWLAWAFV					

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVRFKAE			
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVRFKAE			
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALE				
m259-1	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1   ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTGCGCGGTT  TTTTGACCGC  GCAAACTCTG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CTTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGCTTCGTG  TCGGCGCGTT  CAAAGGCTAA
201 GCGGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCTCTGA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAAAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCAGC  ATTGCCGCCG
401 AGTTGCAAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTGCGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAAACTGACG  GCGGAATATA
551 AAAACATCTT  CGGCGATGCC  TGCCGTTCCG  AAACGGCGTT  GGAGTTGGGC
601 GCGCTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1   MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALVKNHKGK  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVFAD  IFELSAALEG  RAFKGMLKLT  AEYKNIFGDA  CRSETALELG
201 ALNQLQEIS  KTSEKSKRIF  Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVRFKAE			
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVRFKAE			
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
m259-1	VLPDDEDARTIAAELAKMDMFALGTD	AVASGETYGRVFADIFELSAALEGRAFKGMLKLT				
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALEL	GALNQLQEISK	TSEKSKRIFYX			
m259-1	AEYKNIFGDACRSETALEL	GALNQLQEISK	TSEKSKRIFYX			
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTCTT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCAGCATG
101 CCGCTGAATG CGACTTCCTG CCGGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCCGTGGT CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTTCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATTCATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGTGT CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1  MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFPSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFPSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAQVQGPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
a260	AARLFQAFGVNPGAQVQGPAPFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAQVQGPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
a260	AARLFQAFGVNPGAQVQGPAPFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1  atggagcttg ggcataatcgt attccttctg ctttgcgcgc gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctgggacatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctggtcgcgg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatt gatttgacga acacgccgcg
301 gcagtcggga tagcccga aaatcggttc gcacacgccc gcgatgatgt
351 gccgataacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattgga acgccgttgt cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggcctt ggacgttttc gcgccgtag gtttggattg
```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1   ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTGGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CGGCAGTTTC
451 GATGCGGCGG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTCGACG CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1   MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL QQIHQRRVDL KIIVHRQIKG NVHGFQKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	AHARDDVPYP			
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF	AHARDDVPYP			
	70	80	90	100	110	120
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	130	140	150	160	170	180
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1   atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcggtatt ggcaaacgcc ccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgccgcaaa cagcctgacc gccggcgaa gtcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttggcggc aggtaaatct gacgatgcca aactcgcgcc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

607

m263/a263 97.4% identity in 77 aa overlap

				10	20	30
m263.pep				AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE					
	80	90	100	110	120	130
		40	50	60	70	
m263.pep		ELKAFFDAGYNQQQAVEVVMGXLATLCNYVNNLGQTEINPELQAYAX				
a263		ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX				
		140	150	160	170	180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcctc ctcaccgccc cggttcggcac
51  acactccctt cagacggcat ccgcccagcg agtgrtcaag ccggaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgcccgaatt cacgcaaacc
151 ggcaacgcct cgtggtacgg cggcagggtt cacgggcccga aaacttccgg
201 cggagaccgc tacgatatga acgcctttac cgcgcgccac aaaaccctgc
251 ccatccccag ccatgtgcgc gtaaccaaca ccaaaaacgg caaaagcgctc
301 atcgtccgcg tcaacgaccg cggccccctc cacggcaacc gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccg gccaatccgc accggttgcc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggta cggaaacaga
501 agcacaagcc tatctgaacc aagccgccc aaatttcgcc gcttcgcatc
551 caagcccga cctctcgggt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651 acgcggtatg gttcgggcgg tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLG FVS QGTAHV KIEQ IVPGQSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQNFA ASSSSPNLSV EKRRYEYVVK
201 MGPFA SQER AEA EAQARG MVRVLTSG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACGCCG CATTGGGCAC
51  ACACTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAC ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCGCCGAAG CCGAAGCTCA GCGCGCGGT ATGGTTCGGG
701 CGGTATTGAC CCGCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVF GKRYT
51  PKNQVAEFTQ TGNASWYGGF FHGRKTS GGE RYDMNAFTA HKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAAQKLG FV NQGTAVKIE
151 QIVPGQSAPV AENKDIFIDL KSFGEHEAQ AYLNQAAQNF AVSSSGTNLS
201 VEKRRYEYVV KMGPFSQER AEA EAQARG MVRVLTAG*

```

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSF GTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSF GTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGCGCTG ATGATTTTGT CTTGTTTGTT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGCGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCTGAG CTTCGGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAE MPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFVNRGLENVDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI - FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

611

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90     100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATT CCGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTGCGGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACAAGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90     100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGOVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGOVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGOVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
	:::	:::				
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgc actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaat
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggcccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcataatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtcgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgacga
351 tgttgtcgat tatgccgtcg ccgccaaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVDDVDV YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

		10	20	30	40	50	60
		70	80	90	100	110	120
m268.pep		PQT	VQNK	LQPS	QKTW	KSGMD	KICANNAKAEGKTPNGIKFSELACKTAETEARLEELHNRR
a268		PQT	VQNK	LQPS	QKTW	KSGMD	KICANNAKAEGETPNGIKFSELACKTAETEARLEELHNRR
		70	80	90	100	110	120
		130	140				
m268.pep		KALIDEMXREADXKELSKRLX					
a268		KALLDEMAREADKKELPKRLX					
		130	140				

m268-1.seq

1	GTGCAATCCC	GATATGATGG	TTGCATAAA	TTTAAACATA	TATGTTCGCG
51	AGCTATGGCA	CTGATTAAAG	AGCCGTATGGA	CAAAGTGAAA	CAAGAAGGAA
101	AAAGAATTGA	AGCGGCAGAA	GAAGCGGCGG	CGCAGGAGGC	ATTGGGTCCG
151	GACGAGGAAG	CCGCGCCGCT	ATCGCAATGG	GAAGAAGCGC	ACAGAGTGTCT
201	CGCGAGCGAG	TTTGACGACGT	TCTGGAAAGG	ATTGCCTCAA	ACCGTACAGAA
251	ATAAGCTGCA	AGCCTCACAG	AAAACATGGA	AAAGCGGGAT	GGATAATCTC
301	TGTGCCAACA	ATCGCAAGAA	TGAAGGTAAA	AGCCGCAAGC	GCATAATCTC
351	CAGCGAACTG	GCATGGAACA	CGGCGAAAAC	CGAAGCACGC	TGGGAAGAGC
401	TGCAACAACG	TAAAAAGGCC	CTTATCGACG	AAATGGCCAG	GGGAAGCGGAC
451	AAAGAAGAAC	TGTCAAAGCG	GCTCTGGA		

m268-1.pgp

```

1  VQSRDYDLGHR FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAQEALGR
51 EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRI.*

```

m268-1/g268 82.3% identity in 164 aa overlap

				10	20	30
m268-1.pep	VQSR	YDGLHFKFHICSAAMALIKEPLDKVKQRNE	:	:	:	:
g268	KEGAYVVKTIISYSVQPTDDKSKIFAELSQAHDIHPLSELVS--MALIKEPLDKAKQRNE	:	:	:	:	:
	150	160	170	180	190	200
	40	50	60	70	80	
m268-1.pep	ELEAAE-----EAAAQEALGREQEAARVSEWEERYKLRSRSEFEQFWKGLPQTVPN	:	:	:	:	:
g268	KLEAAEATAQEAREAEAAAAQEALGREQEAARVSEWEERYKLRSRSEFEQFWKGLPQTVPN	:	:	:	:	:
	210	220	230	240	250	260
	90	100	110	120	130	140
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEEHLNRKKALIDE	:	:	:	:	:
g268	KLQASQKTWKSMDKICANNAKAEGETPNGIKVSELACKTAETEAREEEHLNRKKALIDE	:	:	:	:	:
	270	280	290	300	310	320
	150	159				
m268-1.pep	MAREADKKELSKRLX	:	:	:	:	:
g268	MVREEDKKELPKRLX	:	:	:	:	:
	330					

a268-1.seq

1	GTGCAATCCC	GATATGATGG	TTTGATAAAA	TTTAAACATA	TATGT1TCCCG
51	AGCAAT1TGCCA	CTGAT1TAAAG	AGCCCT1TGA	CAAGCGGAAA	CAAAAGGCGAG
101	AAGAACTTGA	AGCGCGCAAG	GAAGCGCGCG	CCAGGAGAGC	ATTGGGTCCGG
151	GACGAGGGAAG	TCGACGCGCT	ATCCGAATGG	GAAGAAGCCT	ACRAGGTGTC
201	GCGCAGCGAG	TTCGAGCAGT	TC1TGGAAAG	ATTGCCTCAA	ACCGTACAGA
251	ATAAGCTGCA	AGCCTCACAG	AAAACAT1TGA	AAAGCGGGAT	GGATAAAATC
301	TGTGGCAACA	ATCGCAAGAG	TGAAGGT1TGA	ACGCCAAACG	CGTAAATTT
351	CAGCGCAACTG	GCAT1TCAAAA	CGGCGGAAAC	CGAAGCAGCG	TTGGAAGAGC

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQT  59
               ||||||||||||||||||||||||||||||||||||||||||||
g269          MVWRVNCAATAALIFSSSPWIWAVVWVWSRASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep      ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS 119
               ||||||||||||||||||||||||||||||||||||||||||||
g269          ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTSAALLCLSLRS 120

m269.pep      SX 121
               ||
g269          SX 122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGSCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCGCGGT CCAGCGCGCC GCGGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTGTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTGCG
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVVWWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep      10      20      30      40      50      59
               MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQT
               ||||||||||||||||||||||||||||||||||||||||||||
a269          10      20      30      40      50      60
               MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSWRFCASVPASSAPALTVSPWDFIQT

m269.pep      60      70      80      90      100     110     119
               ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS
               ||||||||||||||||||||||||||||||||||||||||||||
a269          60      70      80      90      100     110     120
               ASPKVSAAALMHSEKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDTSAALLCLSLWS

m269.pep      120
               SX
               ||
a269          120
               SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcggtt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtrgc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgcctgttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgcctgcccc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	LIAFAAV	KLVL	LQWQAX	QPQAVAAQCDL
a270	MNKNRKL	LLAALL	LIAFAAV	KLVL	LQWQAX	QPQAVAAQCDL
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDI	YIEHAP	AGTEQVS	SISFSM	KNMDMG	FNRYMFER
a270	TKKPFDI	YIEHAP	AGTEQVS	SISFSM	KNMDMG	FNRYMFER
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADIT	IGSRTF	QTAFTA	EX		
a270	DFTADIT	IGSRTF	QTAFTA	EX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1   atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttgtg
51  tatggtcagt cctgtgccgg cgttgacgac caagcccaaa tcgccggcga
101 aatgcgcgcc gttttggatg cgctcgaaact gcctgatttg ttcggcggtg
151 ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201 gacatcacgg gcggccttga ttgcctgtc gtcggcatcg ataaacaagg
251 acacgcgtat gcccgcgctc gtcaggattt tggcggaattc ggcgattttt
301 tcctgttgcg ccaatacgtc caaaccgcct tcggtcgtga ttctctgcgc
351 tttttcaggc acgatgcaca cgtcttccgg catcacttta agcgcgtttt
401 cgagcatttc ttccgtcaac gccatttcaa ggttcaggcg cgtgcggatg
451 gcgtttttga cggcaaatac atccgcgtct ttgatgtggc ggcggcttct
501 gcgcagggtg atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551 ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1   MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSAIF
101 SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1   AwGTTCAgTT CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCcGG CGTTGACGAC CAAGCCCAAA TCGCCGGCGA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTtGA TTTGCCTGTC GTCGGCATCG ATAAACAAAG
251 ACACGCGTAT GCCTGCGTCG GTCAGGATTt TGGTGAACCC GGCGATTtTT
301 TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTCGTGA TTTCTGACG
351 TTTTTCAGGC ACGATGCACA CGTCTTCCGG CATCACTtTC AAAGCGTtTT
401 CCAACATTTC TTCCGTCAAC GCCATTtCAA GGTTCAGGCG CGTGCGGATG
451 GCGTtTTTGA CGGCAAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGTAATCA AATCCGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1   XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101 SCCANTSKPP SVVISXRFSG TMHTSSGITL KAFNLISSVN AISRFRRVRM
151 AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

621

	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRKAPCVS					
	: : : : : : :					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRKAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1   atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcaccggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cgaagaattt
201 ttcacgacc aacgagtgca atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcg cgtgaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctgcgggcaa tgcacttcgc tcgcctcgct taccgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgtc gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgtgcacg
701 ccaacagcac caatcaggcg ctgcaccgca tcatcaactt cttccccgag
751 gagcgcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatctcgcaa cgctcgttc cgcgagacgg cggcaagggc aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1   MTAKEELFAW LRHMNKNKGS DLFVTTTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTTC TGACAACCCA TTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACCCTGAC GCGGAAAAA
151 TGTATGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaaACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTGTGCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```

```

a272.seq
1 ATGACC GCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51 CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGAGC AACCGCTGAC GCGCGAAAAA
151 TGTATGAAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCT
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGCT TTGCTCTGCT TATCGCATAC
451 CGCAATGAAA ATTTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCTGGC
551 TGGATACGGA AAATGCGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GACGCGCGCG AACAAATTGCT GACGGATTTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CSGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGTA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG AATCGGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CTTAGTTCCG GTCCCGATTT
1101 GGAAGTGCCT TGA

```

```
a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHTFP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNEFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESNLPPVLK DVALKKRGLV IFVGGTGSCK STSLASLIDY
151 RNENSGFHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLIHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ FLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKRVM KNKSTTLGMQT RDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSQA QSSGPDLELL *
```

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLHRHMKNKGSDFVTTHTFFPAMKLDGKITRITDEPLTAEKCEIAFSIMS					
a272	MTAKEELFAWLHRHMKNKGSDFVTTHTFFPAMKLDGKITRITDEPLTAEKCEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPPVLK					
a272	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIIPKFESLNLPPVLK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIIDYRNENSGHIITIEDPIEFVHEHKNCIITQR					
a272	DVALKKRGLVIFVGGTSGSKSTSLASLIIDYRNENSGHIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180

625

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQGSQ	GKHADRCQD	IGVFKAGT	PFVFLPLL
g273	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQGSQ	GKHADRCQD	IGVFEAGT	PFTVFLPL
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQ	RGRSRARHX	HCVHCCSL	MLKNPPVR	ATVLRRI	QIAKFVCG
g273	AFEIKDDAGKQ	RGRSRARHW	HCVHCCSL	TVKNPPGR	ATVLRRE	IAKFVCGR
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRALCAG	VICRSPAK	SPRTRFA	EFPHCPL	VSYG	VYLPFV
g273	CFXRARPM	CRNIICR	SPAKSP	PRTRFA	EFPRCPL	VSYG
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1   ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAATA
51  CAACGAAAAAT CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC  CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAACT
151 CCATTACCG   TTTTCCTGCC GCTTTTGTG  GCTTTTAAA  TAAAGGATGA
201 TGCCGGCAAG  CAGCGCGGCA GCCGCGCCG  ACATTAGCAT AATGTTTATT
251 GTTGTTTCCTT AACGGTTAAA AACC CGCCG  TCCGTGCAAC CGTTTTTAAG
301 AGGCGGTAAA  TCACAAAGTT TGTTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAAAG GGGCATGATG CACTGCCCCG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC  AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT  CATA CGGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1   MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG  RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL  FVFQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQGSQ	GKHADRCQD	IGVFKAGT	PFVFLPLL
a273	MSLQAVFVYPPSR	TAQYNENQENG	GKAHKQGSQ	GKHADRRQD	IGVFQGTG	PFTVFLPL
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQ	RGRSRARHX	HCVHCCSL	MLKNPPVR	ATVLRRI	QIAKFVCG
a273	AFEIKDDAGKQ	RGRSRARHX	HNVHCCSL	TVKNPPVR	ATVFKR	XITKFVGG
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCAG	VICRSPAK	SPRTRFA	EFPHCPL	VSYG	VYLPFV
a273	GHDALPRV	-PDIICR	SPAKLP	PRTRFA	GFPHCPL	VSYG
	130	140	150	160	170	

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTTCGATTG
451 ACCCCGATGG ACAAACTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274.pep	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cggttcggtt cggtgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaatgg cgcgggcgat
201 ggcgacgcgt tgccgctgtc cggcgataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggtcttga gggcgacag gacttcggct tcgccgcgt cgggacggct
351 gtatcgagc ttttcaaca ggggtgtcgt aaacaggaat acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagttagat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggttg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgtctg atgtcgaggt tgaagtgtc gagggctttg
601 atgccgtctg aacggttatc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgca gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cggcgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTCC GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTG GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRR WATMMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRRWATMMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSI PSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSI PSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

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```

                                     :|||||: |:||:|||||:||||:||||
m277      GLRFVVVELAQQPVGI AVFEVVGGLLDFVLVHVAVG DGVAVERFCPNEVVDVFYTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLG YFHAVEPDFPAQTPRTEGGVFPVVF DKAADV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      RQAFDAVG DFAEYGRAVDAADLLEIGKLG YFHAVEPDFPAQTPRAEGGVFPVVF DKAADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGV EIEVLDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK PRL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      DFGIDAQFAQRVEIEVLDIGSGGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK PRL
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGA AFVCP EQLQFEDDLLEGKHGLL
           ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGA AFVCP ECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTG TTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGCGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGAATAGT GTTGCAAGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGCGGCG
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTCAG TTTGAAGATG ATTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VG DFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GG VFPVVF DKAADVHFGVDA
151 QFAQGV EIEV LDIGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPR LGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCP ECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGI AVFEVVGGLLDFVLVHVAV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPIGI AVFEVVGGLDFVLVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVVDVFYTLQVHRQAFDAVG DFAEYGRAVDAADLLEIGKLG YFHAVEP
           : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVG DFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

```

g278/m278

      10      20      30      40      50      60
g278.pep  LRAITPGAIFSTGAVKVVLIIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC
          |||||
m278      LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC
          |||||

      10      20      30      40      50      60

      70      80      90     100     110     120
g278.pep  SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |||||
m278      SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |||||

      70      80      90     100     110     120

      130     140     150     160     170
g278.pep  DRFSILALIRSLISAGLSCMKTLIRHSRVQSTQFALYRQIQNLITHFNF
          |||||
m278      DRFSILALIRSLISAGLSCMKTLIRHSRVQSTQFALYRQIQNLITHFNFYAANQLRFDF
          |||||

      130     140     150     160     170     180

m278      DRDFQLAVETLIQHLHLQADLFVGQRIGTVNDGRFDMVE*
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

```

a278.seq
1  TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG TCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

```

a278.pep
1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSPTTAPT ESRSRFFIAK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFGVQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

```

      10      20      30      40      50      60
m278.pep  LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC
          |||||
a278      LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC
          |||||

      10      20      30      40      50      60

      70      80      90     100     110     120
m278.pep  SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |||||
a278      SYSPNTTAPTESRSRFFIAKPKVLPGNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT
          |||||

      70      80      90     100     110     120

```

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```

m279.pep      ITICPGELKLTASTTSLWAASQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSLTA
||| ||||| ||||| ||| : ||||| :||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTCSKPKMAAIAPTPCGTADCISSARRRSLTA
              70          80          90          100         110         120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279          SAKSNSAATSAVYSPRLCPATAAGVLPPTSXKX
              130          140          150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1149>:

```
a279.seq
  1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN A GGGCTTCGGC
51  GAGTTTGTCT GCGGGCGGGT TCATGAGGC GAATGGGAA GGTACNGACA
101 CNGGCGAGCG CAGGGCGCGT TTGGCGCCG CTCCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGCGCGCGGC ATTGCCTGCA ATCACGACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NCGCAGCAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCGG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 1150; ORF 279.a>:

```
a279.pep
  1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCF ATAAGVLPPA
151 SE*
```

m279/a279 88.2% identity in 152 aa overlap

```

      10          20          30          40          50          60
m279.pep    ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAMARPTAAALPA
             :| | | | | | | | | | | | | | | | | | | | | | | | | | | | :| | | | |
a279         MTXICGCLISTVVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA
             10          20          30          40          50          60

      70          80          90          100         110         120
m279.pep    ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSTSLTA
             || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a279         ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRSTSLTA
             70          80          90          100         110         120

      130         140         150
m279.pep    SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
             || | | | | | | | | | | | | | | | | | | | | | |
a279         SAKSNAPAATSAVYSPXLCPATAAGVLPPASEX
             130         140         150

```

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

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201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KOVAIIROI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNIFALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSFILGADVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTIAALLATAATAAPLPVVTFSFILGADVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EEGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNPVLM SAYAQNVAKALIKADPEGKVYYQRLGNYQMQ					
	::					
g280	HDHDHDEGHHHDHGEYDPHVWNPVLM SDYAQNVAETLIKADPEGKVYYQRLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAPPAKRKVLTGHD AFSYMGKRYHIEFIAPQGVSEAEP SAKQVA AI					
	::					
g280	LKKLHSDAQAAFNAPPAKRKVLTGHD AFSYMGNRYNISFIAPQGVSEAEP SAKQVA AI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRI AKETGVNVSGKLYSDALGNAPADTYIGMYRHN IK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRI AKETGVNVSGKLYSDALGNAPADTYIGMYRHN VE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGCGC	ACATTAAAAA
201	AATCCGCAGT	GCAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGCGCAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCCT	TATGTCCGCC
451	TATGCCCCAA	ACGTGCGCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCGCCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

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```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcatcc tgtgtccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgacg cgtcctttat
751 cttttttccg tcatactcgg caaagaaggg ggcattctgc ccaaatgggt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGGLWHVI FLILVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCTCGTCA TCGCGCGTAT GAGCCTGA GA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCGC TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GCATGCTGAT
201 GGCACTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCACCTCC TTTTCGGCTC
351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCCTG CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GCGGCGAAA GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
601 ACCGCCCCGC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMLMPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng)

from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG					
	:					
g281	MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGVGG					
	10	20	30	40	50	60
	70					
m281.pep	VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA					
	:					
g281	FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL ISKNGSSVDL LHLLFGSVLA					
	70	80	90	100	110	120
	130					
m281.pep	VDIPALQLIA AVSSLTLITL AVIYRPLVLES IDPLFLKSV GKGGLWHVL FLVLVVMNLV					

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttggtgct
51  gatcaatccg tttagcgcgt tgctgcctta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa ggcgcgcccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcgag
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat ttaaacgcg attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAASV
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCGCG AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAASV
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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```

              70      80      90      100     110     120
m282.pep      GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKONLGAQPETGOARPARNAGAI
a282           GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKONLGAQPETGOARPARNAGAI
              70      80      90      100     110     120

              130     140     150     160     170     180
m282.pep      AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
a282           AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
              130     140     150     160     170     180

              190     200     210
m282.pep      GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFFPQLAGX
a282           GATGLTILNRIMGMMMLAAVSVEIIVSGLKMIFFPQLAGX
              190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1  atgaactttg ctttatccgt catcacattt accctcgccct ctttccctgcc
51  cgtccccgct gccggaaccg ccgtctttac ttggaaagac ggcggcggca
101 acagctattc ggatgtgccg aaacagcttc atccccacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1  MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAGA AGAAACTGC CGGATTTCAG AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRLTRQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

```

              10      20      30      40      50      60
m283.pep      MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTRQTKP
g283           MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP
              10      20      30      40      50      60

```

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```

501 gggtaaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaatcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggatcatc ctttggtgga cgtgaaaaac
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgctgc agtacaacaa ctgtcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcctt ggtcagtttg
851 cgcgcagatt tgccgactgc gccgtcccaa gtggcgaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51 TVFLKAFFLE TFAARFAAEA FFAREMIAAP AAGFPIAPAA FAERLAACGF
101 AFAGRFLHAFD GQFGQFAVNV FFDFVDFDVF VHEGKRNRNT RAACAAGAPD
151 AVDVVFRFLFR QVVVYDVNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LFFDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1 ATGCCGCTCTG AAACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCGTTT GCCTTTGAAG CCTTCGCCGG TTTTTTGA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCCGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGCGG GTCGGTTCCA TGCCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTAAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGC GGCCG GCGCGGCCG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGCG ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGA CGTGAAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCTCT
801 GATCGTCCAC CGGTTTCGACT TCGATGATT CAGGGTCTTT GGTCAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGCGCTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TCGGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAGCAC GCGGCCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51 TVSLKAFFLE TFAARFAAEA FFAREMIAAP TAGFTIAPAA FAERLAACGF
101 AFAGRFLHAFD GQFGQFSVNV FFDFVDFDVF VHEGKRNRNT RAACAAGAPD
151 AVDVVFRFLFR QVVVDNVNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQFAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIORV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

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```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD QQFGQFSNVV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRARAF AKFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSNVV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSNVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRLEFQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRLEFQVVVDNVGNGRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHGDGFDVVDKAHIQHTVGFVQNHQHFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat ttgggcagta

```

649

```

3451 ttctccggct acggcgcgga cgttaccata ggccggcaaac tgaccctgac
3501 cgcgcaaccg ggccggaatg tgcgtggggg gggcacggtc cgcgtcatca
3551 aagggcgtra caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgcgga
3651 acgcccgcct tcccccgctg gtgcgggctg ggaatatatt ggcagcctca
3701 acagcccgcg cttacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcctcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc ggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cgcaaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accgctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1 MTDTPPTDPT PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSJET
101 EGADLKISRF RFAWKPSLML RRSLLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDREFETG KISMGTFFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGASVSG LKKPFALDTA IYTKGGFEFE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPEAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RYNGIPVROVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPO
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRNLNL ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLTG TARNLHIGKA ADIRSLDFTL KGSPTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIKTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSGIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTITSLN ASAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD
951 TAPLGGRLNL TVADAEAFRN FLPVGGTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDND IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGGD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTLLTAQP GGNVRGVGTG RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGAVEIL GSLNSPRITL TANENPMSEK
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRA
1351 QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGGT GGAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACGCCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACGCCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDAPTDT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSEFS DGIALEGSLD LENTHAGFAD RNGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIQIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN ITAPDLRFG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAHVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSLNL QHESWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
 801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD
 951 TAPLGGRLNL TVADAEVFRN FLPVGGQTVKG SLNAAVTLGG SIADPHLGG
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDTPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYYLDREFETGKISMKGAFDK					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPLQGLPDSIDLPAAYYLDREFETGKISMGTFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAAYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFECE					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
g285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep						
g285						

653

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|||||
g285    AAQNITGSLNAsAQICLVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRLNL
          910      920      930      940      950      960

          970      980      990      1000     1010     1020
m285.pep TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSSINGDKLYYRNQTQGIILDNG
          |||||:|||||
g285    TVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSSINGDKLYYRNQTQGIILDNG
          970      980      990      1000     1010     1020

          1030     1040     1050     1060     1070     1080
m285.pep SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
          |||||:|||||
g285    SLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENSVPDVDIGAVFDKYRILSRPNRRLTV
          1030     1040     1050     1060     1070     1080

          1090     1100     1110     1120     1130     1140
m285.pep SGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMPVGGDDVVVLGEVKKAAAPLPVNMN
          |||||:|||||
g285    SGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMPVGGDDVVVLGEVKKAAASLPVNMN
          1090     1100     1110     1120     1130     1140

          1150     1160     1170     1180     1190     1200
m285.pep LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
          |||||:|||||
g285    LTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYGQDLDTKGT
          1150     1160     1170     1180     1190     1200

          1210     1220     1230     1240     1250     1260
m285.pep VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSKDKLSWLILNRA
          |||||:|||||
g285    VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSKDKLSWLILNRA
          1210     1220     1230     1240     1250     1260

          1270     1280     1290     1300     1310     1320
m285.pep GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTKRSRNAQTGELNPAEQVLTVGKQ
          |||||:|||||
g285    GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTKRSRNAQTGELNPAEQVLTVGKQ
          1270     1280     1290     1300     1310     1320

          1330     1340     1350     1360     1370     1380
m285.pep LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
          |||||:|||||
g285    LTGKLYIGYEYGISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
          1330     1340     1350     1360     1370     1380

          1390
m285.pep DSAGNGKGKX
          |||||
g285    DSAGNGKGKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

```

a285.seq
1  ATGACCGATA CCGCACCAGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGCTGCTGAA GCTGTCCGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CGTCTTGGT TCGGCGTAAA CATTTCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGCGAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CAGCCGTGG AGCAGTTCGT CGGGGTCAGC

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655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AACTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

```

a285.pep
1 MTDAPTDTPTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFANKPSELM RRLHTEIS AGDIAIVTKP TPPKEERPPPL
151 SLPDSIDLPA AVYLDRFETG KISMGAFAFK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF DGIALEGLD LENTKAGFAD RINGIPVRQVL
351 GSFVIRQDGT VHIGMTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSST AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTGDDG GKKGDRLNLM I .PDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEEVDL ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSIGI LDIGGAFLNK LQNRMTLEAG AERVAASAA
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFELNVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLLP
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADAEVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRLTV SGNTRLRYS P KGISVTGMI
1101 KTDQGLFGSQ KSMPSVGDD VVVLGEVKKE AAPLPVNMN LTDLDNDGIR
1151 FAGYGADVTI GKKLTLTQAS GGSVRGVGTV RVIKGRYKAY GQDLDTIKGT
1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGVKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKGK*

```

m285/a285 99.4% identity in 1389 aa overlap

```

10 20 30 40 50 60
m285.pep MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
|||||
a285 MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
10 20 30 40 50 60

70 80 90 100 110 120
m285.pep AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
|||||
a285 AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
70 80 90 100 110 120

130 140 150 160 170 180
m285.pep RRLHTEISAGDIAIVTKPTPPKEERPPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
|||||
a285 RRLHTEISAGDIAIVTKPTPPKEERPPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
130 140 150 160 170 180

190 200 210 220 230 240
m285.pep QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
|||||
a285 QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
190 200 210 220 230 240

250 260 270 280 290 300
m285.pep TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAF
|||||

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657

a285	AAQNITGSLNAAAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
	910 920 930 940 950 960
m285.pep	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSINGDKLYYRNQTQGIILDNG
	970 980 990 1000 1010 1020
m285.pep	SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
	1030 1040 1050 1060 1070 1080
m285.pep	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
	1090 1100 1110 1120 1130 1140
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLITKGT
a285	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLITKGT
	1150 1160 1170 1180 1190 1200
m285.pep	VSFVGP LNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
a285	VSFVGP LNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
	1210 1220 1230 1240 1250 1260
m285.pep	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNaQTGELNPAEQVLTVGKQ
a285	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNaQTGELNPAEQVLTVGKQ
	1270 1280 1290 1300 1310 1320
m285.pep	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
	1330 1340 1350 1360 1370 1380
m285.pep	DSAGNGKGKX
a285	DSAGNSKGKX
	1390

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1   CTGAAGCTGT CGGCGGCACT GCTGTCGTGC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCTT
351 GCCCACAGC ATAGACCTGC CCGCCGCCGT CTATCTGCAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGAGCAG TTCGTCGGGG TCAGCCTCGG

```

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1   LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLDDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYYLD RFETGKISMV KTFDKQTVYL
151 ERLNAAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGI GGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSHTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVGRHLSG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLHLQNM
701 TLEAGAEHVA ASAAWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQV DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQONI TGSNLASAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLNTVADA EAFRNFLPVG QTVKGS LNAA
951 VTLGGSIA DP HLGGSSINGDK LYRNRQTGI ILDNSSLSRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIKG
1151 RYKAYQDLDL ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEF MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGVEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSKKDSAGN
1351 GRGK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

```

1   CTGAAGCTGT CGGCGGCACT GCTGCTGTGC CTGATTTTGG CACTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATT CTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA GGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTCCGCGCGG CGACATCGCC
301 ALCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCGCGCGT CTATCTCGAG CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACCGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTGCGGG GCGGCTCGG
551 TCGGCTTGAA AAAACCGTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCG GATGCGGAC TGAATTTGCA CCGTACCGCC ATCCGCTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTGCG TCGATTTGGA AAACACCAA
901 GCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTACGG TTTTAGGCGG
951 CTTTGTATC CGGCGAGGAC GCACGGTGCA TATCGGCAAT ACGTCCGCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATC CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTCCGCG
1551 TGCCGCGGTC GATTGCGGC TGGGGCGGAA CATTATTAAC ACAGACGGCG
1601 GTTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCGGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGAGCG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCGGTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGGCG
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCC
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTC AACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNLRGTLDDGFDGDN
m285-1	LKLSAALLSVLILAVCFLGWLALGTEAGLRFGLYQIPSWFGVNISSQNLRGTLDDGFDGDN
	10 20 30 40 50 60
g285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDS
	70 80 90 100 110 120
g285-1.pep	IDLPAAVYLDRFETGKISMGKTFDKQTVYLERLNAAYRYDRKGHRLDLKAADTPWSSSSG
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	PFAESLDKTLLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
m285-1	PFAESLDKTLLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
	250 260 270 280 290 300
g285-1.pep	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
	310 320 330 340 350 360
g285-1.pep	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGTGTARTDGLAIASDPANEQRKL
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL
	370 380 390 400 410 420
g285-1.pep	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
m285-1	VLDTVNIAAGQGSLSAQGYLELFKDRLLKLDIRSRAFDPSRIDFQLPAGNINGSINLAGE
	430 440 450 460 470 480
g285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLFRAAVDLRLGRNIVKTGGFGKKGD
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLFRAAVDLRLGRNIIKTGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	LDFTLKGSPTSRPMRADIKGGRLSLSGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGK
m285-1	LDFTLKGSPTSRPIRADIKGSRLSLSGGAAVVDTADLMLDGTGVQHRIRTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	PFKLDLDASGGINRELTRWKGSGIGLDIGGAFNLKLQNRMTLEAGAHEVAASAANWQAMG
m285-1	PFKFDLDASGGINRELTRWKGSGIGLDIGGAFNLKLQNRMTLEAGARVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	GSLNLQHFSDWDRKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
m285-1	GSLNLQHFSDWDRKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL
	730 740 750 760 770 780

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCAGCG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TCGCGGCGAA TGGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTTGCGGC TGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAATG TACGCGGACA
1701 CTTTTCCGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCTGTTTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCGCGAC ACAAGCCGCC CGAATCCGCG
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTCT GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG CGGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GATCCCTCGA CATCGCGCGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTTGGA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCACACAG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GCAAAAGCCG CGATGCCGTA TTGCCCAGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACGCGC CTTTCAAAC GACCGTATCG GAATCTGCT
2451 TGACGGCGGC GCGCTTTTCG GCGGATTAAC CGCCGATTTC GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGCAAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCGGC
2601 GCAAAACATT ACCGCGAGCC TGAATGCCCG CGCGCAAAAT GCGCGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCGCCGCTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGGCAGAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTGCGAT ATCGCGGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCCGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCTGTCT CCGCCCCAAC CGCCGCTGTA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAAA
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAACTGACCC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGGCG GCGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CGCTCAACG ACCCAACCT CAACATCCGC GCGCAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GCGTGGAAA TATTGGGCG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACG GCGCCGGCAG TGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCT TTGCGGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAAG CCGCCGCAA
3801 CCGGCAAAAC GCGGAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCGCCGT ATCGGCGGCC GTTCGTGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGAAAC
4051 AGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

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a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
m285-1	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
	430	440	450	460	470
a285-1.pep	490	500	510	520	530
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
m285-1	490	500	510	520	530
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
a285-1.pep	550	560	570	580	590
	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTETDLSGAARNLHIGKAADIRS				
m285-1	550	560	570	580	590
	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTETDLSGAARNLHIGKAADIRS				
a285-1.pep	610	620	630	640	650
	LDFTLKGSPTSRPIRADIKGSRLSLSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGK				
m285-1	610	620	630	640	650
	LDFTLKGSPTSRPIRADIKGSRLSLSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGK				
a285-1.pep	670	680	690	700	710
	PFKFDLDASGGINRELTRWKGSIGILDIGGAFLNKLQNRMTLEAGAERVAASAANWQAMG				
m285-1	670	680	690	700	710
	PFKFDLDASGGINRELTRWKGSIGILDIGGAFLNKLQNRMTLEAGAERVAASAANWQAMG				
a285-1.pep	730	740	750	760	770
	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	730	740	750	760	770
	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
a285-1.pep	790	800	810	820	830
	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1	790	800	810	820	830
	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
a285-1.pep	850	860	870	880	890
	ANAPLGGRITASLPDLGLTKPFLPAAQNIITGSLNAAQIGGRVGSPSVNAAVNGSSNYG				
m285-1	850	860	870	880	890
	ANAPLGGRITASLPDLGLTKPFLPAAQNIITGSLNAAQIGGRVGSPSVNAAVNGSSNYG				
a285-1.pep	910	920	930	940	950
	KINGNITVGQSRSDFTAPLGGRLNLTVAEAEVFRNFLPVGQTVKGSNAAVTLGGSIA DP				
m285-1	910	920	930	940	950
	KINGNITVGQSRSDFTAPLGGRLNLTVAEAEVFRNFLPVGQTVKGSNAAVTLGGSIA DP				
a285-1.pep	970	980	990	1000	1010
	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
m285-1	970	980	990	1000	1010
	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
a285-1.pep	1030	1040	1050	1060	1070
	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
m285-1	1030	1040	1050	1060	1070
	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
a285-1.pep	1090	1100	1110	1120	1130
	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
m285-1	1090	1100	1110	1120	1130
	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
a285-1.pep	1150	1160	1170	1180	1190
	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				
m285-1	1150	1160	1170	1180	1190
	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				

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451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHTR TSGLHRCTRQ
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

```

1  ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACCC
151 GAATCAGTCA AATTAAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAAC GATGCTCCGC AGTAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTTCA AGGCAACCTT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCTG TCAGGACAGT TGGGAAAAACA
551 GCAAACTTTC CGTCTCGGC GCGTAACGC GCAAAGCCTA CCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GCGCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGCACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGGC
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAATAAC GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAACT CGAAACCGGC ATCCGCTCG ATTCGGAATA
951 CCGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAATACGA AACCCAGCTT
1051 GCGCCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCGG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CTTGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCGAAAAC AAAAACTCG
1451 GCACGTTTCA CATAAGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTAGGGCT GATGTTCCGC AGCGCGGCG CGTCTTCGT
1551 GCGCGGTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCCG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTT CACGATATGG GCGATGCCCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTCGGGA CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTTGGC CCGTTTTCCT TCGACATCG CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

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1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLPKFF VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAIVT HITPGPRTKI ANVGVAIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTOAAVN PDTATADLNV VVDSGRPIAF GDFEITGTOR YPEQIVSGLA
251 RFQPGMPYDL DLLDFQQAL EQNGHYS GAS VQADFDRLQG DRVPEKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAVDYNYL FNKGYIGSVV WMDKYEITL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFGSGVWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLTSGAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCACTTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTCAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTAGGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCGGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
  1 MHDTRTMMIK PTALLPALF FFFHAYAPAA DLSENKAAGF ALFKNKSPDT
  51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
 101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAAILGD
 151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
 201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
 251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GASVQADFDR LQGD RVPVKVSVT
 301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WDMDKYETTL
 351 AAGISQPRNY RGNWYTSNVS YNRSTQNLK KRAFSGGIWY VRDRAGIDAR
 401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNVL HPENGHYLDG
 451 KIGTTLGAFI SSTALIRTSR RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
 501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
 551 FTRTLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
 601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

      10      20      30      40      50      60
m286.pep MHDTRTMMIKPTALLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVK LKPKFP
          |||
a286      MHDTRTMMIKPTALLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVK LKPKFP
          10      20      30      40      50      60

      70      80      90      100     110     120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
          |||
a286      VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
          70      80      90      100     110     120

      130     140     150     160     170     180
m286.pep LTEKDGAITVHITPGPRTKIANVGVAAILGDILSDGNLAIEYRNALENWQQPVGSDFDQDS
          |||
a286      LTEKDGAITVHITPGPRTKIANVGVAAILGDILSDGNLAIEYRNALENWQQPVGSDFDQDS
          130     140     150     160     170     180

      190     200     210     220     230     240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
          |||
a286      WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
          190     200     210     220     230     240

      250     260     270     280     290     300
m286.pep YPEQIVSGLARFQPGMPYDLDLLLDFQQALEQNGHYS GASVQADFDR LQGD RVPVKVSVT
          |||
a286      YPEQIVSGLARFQPGTPYDLDLLLDFQQALEQNGHYS GASVQADFDR LQGD RVPVKVSVT
          250     260     270     280     290     300

      310     320     330     340     350     360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWDMDKYETTLAAGISQPRNY
          |||
a286      EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWDMDKYETTLAAGISQPRNY
          310     320     330     340     350     360

      370     380     390     400     410     420

```

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```

151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARSRRLPA
251 EIPLIPVNOA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDGIIDSG DDLHMGTKKF KAAIDGNGFK GTWTENGSGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  GTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTTCCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AATCAATCAA GCCGCCGTTT
551 CTTCAGATCC CATCCCCGCG TCAAACCTTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGGA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTGA AAAATTAAAT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTACG CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAA TCTGTGACG GCATTATCGA
1251 CAGCGGCGAT GATTTCGATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1  MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSPAP VVSEKETEAK
51  EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFGRLDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFEVL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLT
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQFK AADGNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVSE-----KETE
          |||||
g287      MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVAENAGEVLPKEKKDEEA
          10      20      30      40      50      60

```

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```

801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTTCAG GCGTTCTGCA CGGTCGAGGC GGTGCGCTTC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTTC
1001 ATGGGGAAGC GGTCAGCCTG ACGGGGCATT CCGGCAATAT CTTCCGCCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCCAACC GGCAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGGTGTACAAC GGCGAAGTGC TGCATTTCCA TATGGAAGAC
1201 GGCCGTCCGT CCCCCTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTTCGG
1251 CAGCAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGAA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CGGCGTGTTC GCCGGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

```

a287.pep
1 MFKRSVIAMA CIVALSAACGG GGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQGGDPSAG ENAGNTADQA ANQAENNVQV GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VYIKDKSAS
301 SSSARFRRSA RSRRLPAEM PLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEH
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSKPAAPVVTEDEVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGGAPSAGSQSDMAAVSEENTGNGGAVTADNPKNEDVAQNMPQNAAGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATDNPENKDEGPQNDMPQNAADT
70 80 90 100 110

110 120 130 140 150 160 169
m287.pep DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDPSAGGQNAGNTA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDPSAG-ENAGNTA
120 130 140 150 160 170

170 180 190 200 210 220 229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DQAAANQAENNVGGSQNPASSTNPNATNGGSDFFGRINVANGIKLDSGSENVTLTHCKDKV
180 190 200 210 220 230

230 240 250 260 270 280 289
m287.pep CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
a287 CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVYIKD
240 250 260 270 280 290

290 300 310 320 330 340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
| :| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
a287 KSASSSARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
300 310 320 330 340 350

```

675

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

```

      10      20      30      40      50      60
m288.pep  MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          |||||
g288      MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          10      20      30      40      50      60

      70      80      90      100     110     120
m288.pep  RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          |||||
g288      RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          70      80      90      100     110     120

      130     140     150     160     170     180
m288.pep  PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF
          |||||
g288      PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADVFVACTQVF
          130     140     150     160     170     180

m288.pep  DTX
          |||
g288      DAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51 TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCCT GTGCTGCCAA AGCAGCCATC GCGGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCGCGCG TTAACCGGCA TTCTACCTTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCCGC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

```

      10      20      30      40      50      60
m288.pep  MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          |||||
a288      MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGGLPHIVTKCAV
          10      20      30      40      50      60

      70      80      90      100     110     120
m288.pep  RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          |||||
a288      RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV
          70      80      90      100     110     120

      130     140     150     160     170     180
m288.pep  PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF
          |||||

```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1  ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51  QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
g290                                PQAAYITEAVRRGDISRTVSATGEISPSNLSVSVGAQASGQIKKLYVKLGQVKKGDLIAE
30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g290                                INSTTQNTNIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD
90      100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g290                                ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAI PVEEGQTVNAAQST
150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g290                                PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g290                                GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g290                                KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKECDKVVISEITAAEQQESGERALGG
330     340     350     360     370     380

m290.pep                                PPRRX
|||||
g290                                PPRRX
390

```

679

```

m290.pep      GGYNSSTDASNAYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||
a290          GGYNSSTDASNAYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               : |||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg *cctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgcgaacgcc gaatccgcgcg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcgct
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgcgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgcgcgcg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccgga ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatcc cgtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgcca
701 cccttcgtct tcccaacgg gcgcaccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAVASLKR
51  LEKTYSAQDL KVLVSVETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLT EE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNFVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPDA
251 PTGGNHPPKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAaaaaa CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSAVASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFEN GTPTLVFPNG RSQSGYSMP
251 QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292.pep MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSAVASLKAR LEKTYSAQDL
a292      MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSAVASLKAR LEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292.pep KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
a292      KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292.pep ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
a292      ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292.pep ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQGFEN GTPTLVFPNG
a292      ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQGFEN GTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292.pep RSQSGYSMP QLEEIIRKNQX
a292      RSQSGYSMP QLEEIIRKNQX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtcctggtc
51  gggttcgggt gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcagcgcct
151 tggcatcggg tgccggcggt caagtcgaat cggcggacgc gtggcgtgaa
201 gccgttgaaa aaaccttata tggcgagggg ggcgggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcggggggcg atagtgtatc
351 aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgcg
451 tttttgaag tgctggtttt gtcggtcctg catacgggac ggggtgtcgcg
501 cgaggcgagg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcgga ctgctgttcg ccaggggaa ctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFP ALRRYSAPRP TIFPKPAGTP
51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRAWTALS HNIAERAPES
101 PRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFAVG LLFARGTLES
201 TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

683

```

701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

```

a294.pep
1  MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPRP TIFPKPAGTP
51  WRRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSCAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

```

m294/a294 94.9% identity in 277 aa overlap

m294.pep	10	20	30	40	50	60
	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAPRP TIFPKPADTPWRRVRRFKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAPRP TIFPKPAGTPWRRVRRFKSN					
	10	20	30	40	50	60
m294.pep	70	80	90	100	110	120
	RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI					
a294	RRTRGGKPLKKTYRPRRAECRCRRARTALSHNIAERARESPRRYGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
m294.pep	130	140	150	160	170	180
	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSRARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSCARREVEKAMSYR					
	130	140	150	160	170	180
m294.pep	190	200	210	220	230	240
	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
a294	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240
m294.pep	250	260	270			
	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

```

g295.seq
1  atgctcggga tggcgcgga cgacggccag cagggcatcg ccgcgatatt
51  gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gttttcaaaa
151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
201 tattgccgca cacctgcacg gatgcccgcg ccaatttcgc caaccgcgcc
251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
351 gccgcgcatt cgccaaaaac agcggcacac ccgctgcggc gcattccttc
401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggag
451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
501 agcggcattg cgcacgggga aacagaactt gcgcggtttc ccgtcccgtc
551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaaa gccgccgcaa
601 ctgcgctatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt
651 gtatccaaac cgcgcgggta acgggattcg gatcgggctt gccgaaacgc
701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtccaa
751 ataacgccgt atccatatcg gcgcaagcag ccaataca tcataaagcc
801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacggttc
851 ggacggcatt tcggcaacgg aatcaaatat cgtag

```

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1   ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCGA CGGCATCAGG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGCGGCGAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGCG AAAAAGTGGC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCGGTA ACGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTTCGGAGC GTTGTGCTAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTTGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1   MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSGGR
101 TDQAADFQIT V*RFRRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHR
151 VFAQKLPYPR FVIRKIAAL CIRKQNLGRF PSRRGHLRHQ QRRIGKTLQP
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLG	MARHDDQ	QRI	AAILLPR	RQOFFRLVFT	PINARAAAHGNRPASDAFFKLPRQRFHLFR
a295	MLG	MARHDDQ	QRI	AAILLPR	RQOFFRLVFT	PINARAAAHGNLPVSDAFFKLPRQRFHLFR
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVFGLIA	HLHGCRAQFR	QPRRIRLCL	RQTPRQSGGR	TDQAADFQIT	VQRFRRQPRI
a295	RHQVVFGLIA	HLHGCRAQFR	QPRRIRLRLC	QTARQSGGR	TDQAADFQIT	VXRFRQPRI
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQKLP	YPRFFVIRKIA	ALRIGKQNLGRF
a295	RQQRHTRAP	AFHLQIGP	DFGFHQNAE	HRAVFAQKLP	YPRFFVIRKIA	LCIRKQNLGRF
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	P	PRRGHLRHQ	QRRIGKTP	QLAYQGLG	TRFSDRNGV	YPNRAGNGIRIRLAETLVPMRPI
a295	P	SRRGHLRHQ	QRRIGKTL	QLAYQRLG	TRFPDRNGV	YPNRAGNGIRIRLAETLAPMRPI
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	C	RGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	XTVQTAFRQRNQISX
a295	C	RGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	RTVRTAFRQRNQISX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

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201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDDEGKV LOEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTVPRA SADGVITFKG RKGgyGNAMV IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQQRVEQNLPLPSWGGSGVQT
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQQRVEQKLPLPSWGGNGVQT
m297.pep	AYVWQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA
g297	AYVWQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRRSASEADMKVLPTLRVSVVVKTSARGSLARAEVVP
g297	REVQFFTDDEGERNLVALEKKGGIWRRSASDADMKVLPTLRVSVVVKTSARGSLARAEVVP
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAFY
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAFY
m297.pep	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
g297	YRSDKEGGGGNYYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
m297.pep	AAPQGTVPRASADGVITFKGRKGGYGNAMVIRHANGVETLYAHLSAFSQAEGNVRGGEVI
g297	AAPQGTVPRASADGVITFKGRKGGYGNAMVIRHANGVETLYAHLSAFSQAQGNVRGGEVI
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKOKADALLARLR
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKOKADALLARLR
m297.pep	GIPVTVSQSDX
g297	GIPVTVSQSDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGACG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTGG	TCGGCGGCGA
351	CGGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGA AAAA	AAAGGCGGCA	TATGGCGCGC	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

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```

          370      380      390      400      410      420
m297.pep  GFVVGSTGRSTGPHLHYEARINGQPVNPNVSVALPTPELTQADKAAFAAQKQKADALLARLR
          |||||
a297      GFVVGSTGRSTGPHLHYEARINGQPVNPNVSVALPTPELTQADKAAFAAQKQKADALLARLR
          370      380      390      400      410      420

          430
m297.pep  GIPVTVSQSDX
          |||||
a297      GIPVTVSQSDX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTC CCGCCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcggcgac ggCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAAACAAGG CACCGAAGCC GCCCGCTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTCTGCTGAT GCAGGGCGTT GCGCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTG CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAAGTCTTT CGGAACATT GAAAGGCAAA ATCATCTGA TTCCACCGC
801 GCAAAACTG AGCGGCGGGA AAGGCGGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATG -

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKIFL SGETPPTAQD GGSADMPPEA AASEAAPPAG
101 GTEWKQGTGA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGNPDW WDFPVGKRYL
201 KFADEWAQAE YLKRVDRILE AAHTRVQVW WLGIPLYMKV KLDGQMYRLD
251 KLLSEHLKGG IILIPTAQLT SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCGCCGAC GGTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCT TCAAACCGGT
301 GAAACAGAAT GGAAACAAGA CACCGAAGCC GCCCGCTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGGCGTT GCCCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTG CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAAGTCTTT CGGAACATT GAAAGGCAAA ATCATCTGA TTCCACCGC
801 GCACACCCCT AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

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```

751  AAACGCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCACCGGC
801  GCACACCCTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAGAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKV  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151  KQSTGLSYPS  FFDWPKTIE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201  KFASDEWAE  YLKRVDRI  LEAAHTRVQV  WLGIPYMKKA  KLDGQMRYLD
251  KLLSEYLGK  IILIPHTA  HLTSGGKDRY  TDSVNVNGK  PVRYRSKDG  IHFTA
301  EGQKLLAAK  IMEKIVFE  PSTQPSSTQP  *

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFSLGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFSLGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTTEAAAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFADEWAEYLRVDRILEAAHTRVQVWLGIPYMKKA					
a298	LAVFLGPNDPWDFPVGKRYLKFADEWAEYLRVDRILEAAHTRVQVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGIILIPHTHTLSGGKDRYTDSVNVNGKPVRYRSKDG IHFTA					
a298	KLDGQMRYLDKLLSEYLGKIIILIPHTHTLSGGKDRYTDSVNVNGKPVRYRSKDG IHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA  AACACTTCAT  CGCATTTTCC  GCCCTGTTCC  CCGCCACGCA
51  GGCAGAAAGC  CTGCCCGTCG  CCTCCGTCAG  CCCCAGACAC  GTTACCGTTT
101  CCCCCTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCCGCCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGCGCAG  GCCTTCGCCT  TCCTGCAAA  TCGCGACTCG  CATACCGCCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAA  GCCTGCAAAA  AACATGGGGC
301  GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GGCGGCGGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTCCCGCTC  GGCGJCATCC  TCGCCCAAAC  CGGACGCGGC
451  GGCGGCATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVSPSPAPYTDTHGLLDYGNAAASPWMKK
	10 20 30 40 50 60
m299.ppe	LQSV AQSGSETFRILQIGDSHTAGDFFDLSLRRLQKTWGDGJIGWVYPANVKQQRMAAV
	70 80 90 100 110 120
g299	LRSAVQSGSEAFRILQIGDSHTAGDFFDLSLRRLQKTWGDGJIGWVYPANVKQQRMAAV
	70 80 90 100 110 120
m299.ppe	RHNGNWQSLTSRNNTGDFPLGGI LAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFTRNNTGDFPLGGI LAQTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.ppe	TVNGNTVSANGGGQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.ppe	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.ppe	LIIGAPESLKNLTGVCGRTPVRLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGRTPVLLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.ppe	GWAAKDGVHFSAGYRRAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATT TTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCCGTC CGGCACAACG GTAAC TGGA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTGCTC GGCGGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTCAGCA TGAAAACTG GCTCAACCAC GGATGGGCGC CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGCGGGA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGT CGCTCCGCTG CAATCAGGCA ATAA

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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAATGG TTTTTTATGG
701 CAGCCAGTAC GTTGTGATG GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGGCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTATT TTCTTGTGT
1001 TTGCGCTGCC GGGCATTTGT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCT GGCTGATTAT GGCAGCGCTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATCTT JCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:
g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDP RPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFIILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKGDAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLVGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

```

m302.seq
1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTTACGCTT TTTATATTTT TCATGTGTGT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGAATA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGTTTTT ATCAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAAT CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAAATC ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCGT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTAGC TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAATCACG CCTTTGGAAT ATAAAGGATT AATTGGGGCT GCGGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGTTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTATTTT TCTTGTGTG TGCATGyCG GGCTTTGTTT
1001 ATGGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CgTAATGCG

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVPLKEVGLGGSVLFIFIGILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIAQAYRIGDSVTNIIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIAQAYRIGDSVTNIIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGPTPTFFYPVFX
          490      500      510      520      530

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGCGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATT CTATGATGT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTGTG
1551 TTTGGGCTG CCCGTCGGT CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILHTVKVN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTFMVFVFTG

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g305.seq
 1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCTG
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CCGTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTTTG GCGGTTTTT TTATTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
 451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
 501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
 551 CGGCAACGGA GTTTTCATT TTCTGGCCG TTCCGATGAT GGTGTCAGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT TTGATAGGCT TTATGCTGC TTTTGTTCG GGTGTTGTAG
 701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
 751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
 101 DKQIKEXLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
 251 AYYRIVFGIV IILWLSGWI SWE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)
 1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCTG
 101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CAGTTTGGC GGTAGTGTG GAATACCGGC AACGTTTCAG
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
 301 GGCawACAAA TCAAAGAGyA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
 501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
 551 CTGCGACAGA ATTCTCGTTT TTCTGGCTG TGCCGATGAT GGTGCGCGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT CTGATAGGCT TTATGCTGC CTTTGTTCG GGCTTGGTAG
 701 CGGTAAAAGC GTTGTGAGG TTTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF
 101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSN HKVFEIAIQ LGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSN HKVFEIAIQ LGAVLAVVF					
	10	20	30	40	50	60

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	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPK	IADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI				
a305	GGFFILWVEKRSRAEPK	IVDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI				
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCACAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGAAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAAG  AAATGAAAAA  CTTTGGGCAA  GCGGAAGCC  AACGCATTAT
651 CTGCAATGAG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGCGCG
751 GACATAAAAC  GCTTTACCGC  GTGCAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  QQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRE
251 DIKRFTACKA  AICPPMR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTGTTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAwGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGACGCG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAW  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

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601 GAAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
751 ATAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KLSGFFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD QQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                  GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK
a306              MFMNKFSQSGKLSGFFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                  10      20      30      40      50      60

m306.pep          50      60      70      80      90     100
                  NQXKEDIQPKPADQNALSEPDAAEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP
a306              NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                  70      80      90     100     110     120

m306.pep          110     120     130     140     150     160
                  GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
a306              GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                  130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                  TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTRARKGSVPNWQSWAY
a306              TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                  190     200     210     220     230     240

m306.pep          230     240     250
                  LPRWSVIRRDIKRFTGCKAAICLPMRX
a306              LPRWSVIRRDIKRFTGCKAAICLPMRX
                  250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gacccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaaact aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgta acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFQH
101 KPYLDDFKKE  HNLDITEVFO  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      OWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSOWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAX
              |||||
a307      AWNEGAAX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTTCAC  TATAATAGCC  GGTGTCCTG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGC
451 GCGGATGTGG  TTTTGAAGGA  AAGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADVFHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPLE  NLAHLDNMKR  VTEMGGVVP  PVPAMYRKPQ
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCT  GTTTTTTCAC  TATAATAGCC  GGTGTCCTG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAAGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

707

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRV	FYRIL	GVADNLYPRL	SDFCFF	TIAGLPLQAVL	WERMMVRR
a308	MLNRIF	YRILGVADNLYP	YLSDFCFF	TIAGLPLQAVL	WERMMVRR	LIIGISGASGFQY
	10	20	30	40	50	60
m308.pep	GVKALELL	RAQDVETHLVV	SKGAEMARASE	TAYARDEVYALAD	FVHPIGNIGACIAS	SGTF
a308	GVKALXLL	RAQDIETHLVV	SKGAEMARASE	TXYARDXVYALAD	XVHPIGNIGACIAS	SGTF
	70	80	90	100	110	120
m308.pep	KT	DGMLVAPCS	MR	TLASVAHGF	GD	NLLTRAADV
a308	KT	DGMLVAPCS	MR	TLASVHGF	GD	NLLTRAADV
	130	140	150	160	170	180
m308.pep	KT	DGMLVAPCS	MR	TLASVHGF	GD	NLLTRAADV
a308	KT	DGMLVAPCS	MR	TLASVHGF	GD	NLLTRAADV
	190	200	210	220	230	
m308.pep	X	TEMGGVVFP	VP	PAMYRKPQT	AD	DIVAH
a308	V	TEMGGVVFP	VP	PAMYRKPQT	AD	DIVAH
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTAAATC GGGTATTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGTGTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 TGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCCTGT TCGATGCCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFIIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPQ
201 TADDIVAHSI AHTLSLFGID TPLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTAAATC GGGTATTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGCGTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFIIA GLPLQAVLWE RMMVRRLLI

```

709

```

m308-1      KTDGMLVAPCSMRILASVAHGFGDNLTRAADVVLKERRRLVLMVRETPNLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKQPTADDIVAHSVVAHALSLFGIDTPDSEWQGMADX
              |||
m308-1      VTEMGGVVFPPVPAMYRKQPTADDIVAHSVVAHALSLFGIDTPDSEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1  atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccc gcgcgctttg ggggtgtttg
101 gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcy gcattctgat tgaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccc ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggttcg
601 gaacgttttt tgctgttggg aggcgggaac agccggtcca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgcgccttt gggcgcggag tgggcggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cgttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cacggccgtt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggccggcgcg cgaaagtcgc
1251 cgaagccctg ccgctgcat ttttgccgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1  MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILITV RAGGKTVAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVK GVDGRGVHLHLE TAEGEQTVVS GEISLRPDNR SVSVKRPDS
201 ERFLLLEGGN SRLKAWAVEN GTFATVGSAP YRDLSPLGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFSS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNASVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTGCGCCT GTTGCGGCAG TGGCGTGTCT GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCAATTAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACCGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CTGnCGAAG CCGCGGGATT

```

711

```

                240      250      260      270      280      290
m311.pep      WFNALGSRFRSRNACVVVSCGTAVTVDDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                |||||
g311          WFNALGSRFRSRNACVVVSCGTAVTVDDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                300      310      320      330      340      350

                300      310      320      330      340      350
m311.pep      HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA
                |||||
g311          PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIITGGGAAKVAEA
                360      370      380      390      400      410

                360      370      380      389
m311.pep      LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH
                |||||
g311          LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
                420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTCAAGT   TTGGCTGGGT   GTTTGACCGG   CCGCAGTATG   AGTTGGGTTC
51  GCTGTCGCCT   GTTGCGGCAG   TGGCGTGCCT   GCGCGCTTGG   TCGCGTTTGG
101 GTTTGAAAC    GCAATCAAG    TGGCCAAACG   ATTTGGTCTG   CGGACGCGAC
151 AAATTGGGCG   GCATTCTGAT   TGAACCGGTC   AGGACGGGCG   GCAAAACGGT
201 TGCCGTGGTC   GGTATCGGCA   TCAATTTCTG   GCTGCCCAAG   GAAGTGGAAA
251 ACGCCGCTTC   CGTGCAATCG   CTGTTTCAGA   CGGCATCGCG   GCGGGGAAAT
301 GCCGATGCCG   CCGTGTGCT   GGAAACGCTG   TTGGCGGAAC   TTGATGCGGT
351 GTTGTGCAA    TATGCGCGGG   ACGGATTTGC   GCCTTTTGTG   GCGGAATATC
401 AGGCTGCCAA   CCGCGACCAC   GGCAAGGCGG   TATTGCTGTT   GCGCGACGGC
451 GAAACCGTGT   TCGAAGGCAC   GGTAAAGGCG   GTGGACGGAC   AAGGCGTTCT
501 GCACTTGGAA   ACGGCAGAGG   GCAAACAGAC   GGTGCTCAGC   GCGGAAATCA
551 GCCTGCGGTC   CGACGACAGG   CCGGTTTCCG   TGCCGAAGCG   GCGGGATTTC
601 GAACGTTTTC   TGCTGTTGGA   CGGCGGCAAC   AGCCGGCTCA   AGTGGGCGTG
651 GGTGGAAGAA   GGCACGTTTC   CAACCGTCGG   TAGCGCGCCG   TACCGCGATT
701 TGTCGCCTTT   GGGCGCGGAG   TGGCGGAAA    AGGTGGATGG   AAATGTCCGC
751 ATCGTCGGTT   GCGCGGTGTG   CGGAGAATTC   AAAAAGGCAC   AAGTGCAGGA
801 ACAGCTCGCC   CGAAAAATCG   AGTGGCTGCC   GTCTTCCGCA   CAGGCTTTGG
851 GCATACGCAA   CCACTACCGC   CACCCGAAG    AACACGGTTC   CGACCGTTGG
901 TTCAACGCCT   TGGGCAGCCG   CCGCTTCAGC   CGCAACGCCT   GCGTCGTCGT
951 CAGTTGCGGC   ACGGCGGTAA   CGGTGACGCG   GCTCACCAGT   GACGGACATT
1001 ATCTCGGGGG   AACCATCATG   CCCGGTTTCC   ACCTGATGAA   AGAATCGCTC
1051 GCCGTCCGAA   CCGCCAACCT   CAACCGGCAC   GCCGTAAGC   GTATCCTTT
1101 CCCGACCACA   ACGGGCAATG   CCGTCGCCAG   CGGCATGATG   GATGCGGTTT
1151 GCGGCTCGGT   TATGATGATG   CACGGGCGTT   TGAAAGAAAA   AACCGGGGCG
1201 GGCAAGCCTG   TCGATGTCAT   CATTACGGGC   GCGGCGCGCG   CAAAAGTTGC
1251 CGAAGCCCTG   CCGCTGCAT   TTTTGGCGGA   AAATACCGTG   CGCGTGGCGG
1301 ACAACCTCGT   CATTACGGG   CTGCTGAACC   TGATTGCCGC   CGAAGGCGGG
1351 GAATCGGAAC   ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR   PQYELGSLSP   VAAVACRRAL   SRLGLKTQIK   WPNDLVVGRD
51  KLGGILIETV   RTGGKTVAVV   GIGINFLPK   EVENAASVQS   LFQTASRRGN
101 ADAAVLLETI   LAELDAVLLQ   YARDGFAPFV   AEYQAANRDH   GKAVLLLLRDG
151 ETVFEGTVKG   VDGQGVHLE   TAEGKQTVVS   GEISLRSDDR   PVSVPKRRDS
201 ERFLLLDGGN   SRLKAWVEN   GTFATVGSAP   YRDLSPLGAE   WAEKVVDGNVR
251 IVGCAVCGEF   KKAQVQEQLA   RKIEWLPSSA   QALGIRNHYR   HPEEHGSDRW
301 FNALGSRFRS   RNACVVVSCG   TAVTVDDALD   DGHYLGGTIM   PGFHLMKESL
351 AVRTANLNRH   AGKRYPFPTT   TGNASVSGMM   DAVCGSVMM   HGRLKEKTGA
401 GKPVDVIITG   GGAAKVAEAL   PPAFLAENTV   RVADNLVIH   LNLNIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTTGA AACGGCAGaa ggcGAACAGa cggtcGtcag
951 cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGGcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGGcCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGTCTCGTC TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTGCGAA GCGGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP OHVSQLAREA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECIMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVGDG
301 RGVHLHLETA GEQTVVSGEI SLRPDNRVS VPKRPDSERF LILEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWFNA LGSRRFRSRA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFPFTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVIIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGCGA CATAACGCGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGGCGC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 TCGGATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGACAAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAAGTGGTC CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA GTGGCGGTGC GGCGCGCCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGCG
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTTGA AACGGCAGAG GGCAACAGAG CGGTCGTGAG
951 CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCTGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCG GTTGTGAAC ATGATTGCCG

```

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1       VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLNLI A AEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1   ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGAATCACCT
351 GCAAAATAAG GGCAGGGGGC GTCAGGGGCG GAAGTGGTCG CACTGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA GTGGCGTGCC GCGCGGCCTT
501 GTCCGCTTTG GGTTCGAAAA CGCAAAATCA GTGGCCAAAC GATTGGTTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCTG TGTGCCCCAA
651 GGAAGTGGAA AACGCCGCTT CGGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGGGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTGTATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGCGGCTT TGCATTGGA AACGGCAGAG GGCAAAACAG CGGTCTGTAG
951 CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGGGGGATTG GGAACGTTT CTGCTGTTGG ACGCGCGCAA CAGCCGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCGCGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGAGCC GCCGCTTCA CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACCGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCA AACGGGCAAT GCCGTCGCCA CGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1   MTLVKPSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGROGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTOIKWPN DLVVGRDKLG GILIVRTVG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEETVRGVDG
301 QGVHLHLETA GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPLGAEMAE KVDGNVRIWG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHEP EHGSDRWFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHH YLGGTIIMPGE HLMKESLA VR TANLNRHAGK
501 RYFPPTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTLVKPSHWRVLAELADGLPOHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
              |||||
m311-1       MTLVKLSHWRVLAELADGLPOHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQTALKHECAS...DEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1       LVRPLAVFDAEGLRELTERS GFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

```


717

```

901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCGCGCGA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCGGT TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTGGGGC TACGCGCCTG TAATGCCGCG AAAAGAAGGT TCGTGCGAAG
1301 TGTTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMWADRNF DVRTITIGID LHDICISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQIRISVT PIAQIAAATK ADSYVSVQAQT
101 LDKAAKAIGV SFIGGFSAIV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCGGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTGCGcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAATTTGT CGTGTCTTGC AACCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCGCGCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGCCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAATC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTCCGG CATATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMWADQNF DVRTITIGID LHDICISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQIRISVT PIAQIAAATH ADSYVSVQAQT
101 LDKAAKAIGV SFIGGFSAIV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FCGAKIVVFC NAVEDNPFXA
201 GAFHGSQDAV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIIVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGLLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

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```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTATGCGG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGGT
651 ATCCGGCCCG GGTGTCTGTA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCGCGCA CACCATTTCG GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCGCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
1  MSIQSGEILE TVKMOVADQNF DVRTITIGID LHDICISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDVSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312       MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFFIGGFSALV
          |||
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFFIGGFSALV
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEV LIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGEVKRTAEITPEG
          |||
a312       QKGMSPSDEV LIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPGVVKAALENS DATTLTEVAE
          |||
a312       FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPGVVKAALENS DATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTFPVGDVSVARILEEMGLSVCGTH
          |||
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDVSVARILEEMGLSVCGTH

```

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

```
a313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGCGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCACAAAC TGCCTTGCTC
301 TGC CGCTTGA TTTGGCTTGT GATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TCTTGGATT TCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA
```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

```
a313.pep
1  MDDPRTYGS NPGATNVLR S GKKKAAALT L LGDAAKGLV A VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGV L LALSPTTALV
101 CALIWLVMF QFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNILN LIKGESKIG EKR*
```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFQFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGESKIGEKRY					
	130	140	150	160	170	

723

```

      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.ppep HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
g401  HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.ppep NKSELDAVVAYLQGLGLALKNVRX
      |||
g401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCAGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCG TGCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAATAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.ppep
1  MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF PLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.ppep MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN ALQVAGRDIY
      |||
a401  MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN ALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.ppep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.ppep HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
a401  HRIHLLNPRDVVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.ppep NKSELDAVVAYLQGLGLALKNVRX
      |||
a401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

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725

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651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TagGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CCGCATCGAA CGTGCCTATC TGCTACCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAA+ CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATT GGCCGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVFPQAFSFTLACFLTGIAGV					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVFPQAFSFTLACFLTGIAGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQIQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDPRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					

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51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAV
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNNTSLIYMXSFLSGLLSLGIEVLWVRMFSAQSVPAESFTLACFLTGIAVG					
a402	MDIVNTKPNNTSLIYMLSFLSGLLSLGIEVLWVRMFSAQSVPAESFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
a402	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

729

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51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYETT AETTSGLTGT LTTSLSLTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGQP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT					
m406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTTSLSLTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFSIDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFSIDIQPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

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101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggg cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggg caacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgat acgtgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaacgga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcggcgga
651  taatttcgcg tttcagttcg tcgtcttgtt tgtcaaatc caacaaggct
701  ttcgggtgga tgcgatttg gcggtgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggctcgatt gccgcagccg acgacggcag gaataccacg ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccg atcggtcatg tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cgggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcagcgc cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cgctgcctt
1251 cttcttggga tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagt
1351 tttttcgatg gtcagcgcgt agtgtgccaa ctcgggtgat tcttcgtcgg
1401 taatggagaa gcggttcggg tcttcttcgg ggaattcgac gttggttacc
1451 gatattgcgg cttcggcttt gtcggtgaaa atcattttga tgtgttcga
1501 acccatgggt ttgcgcagga tggcggggtt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```

g501.pep
1  MVGRTLTA DT DIFVLLAAGG DGKMQHHFDG RVAFVKRF GH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFGFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFVRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDBG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLLALD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAAFLLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDLVLVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

```

m501.seq
1  atggtcggac sggccttgac cgcagatgcc gacatatttg tctcgttcg
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgaggg
151  cagttgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggg cgtttttgcc gcgttccaag ccgttttctt tcagggcttt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgat acgttgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaacgga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttgtt tgtcaaatc caacaargct

```


733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLVFKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHDFDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNAQFTRDGGVAGTAAAVGNDGRSTFHHGFPIR
	310 320 330 340 350 360
g501	IAFGTGYGNFLTTFVQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGGSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGAAFAXYGFVAVDGEAAQVAVALFLG
	370 380 390 400 410 420
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGTTFAQDGFFAVDGVAAQVAAAFFLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVMRQLSNFFVGNGEAVAVFLGDID
	430 440 450 460 470 480
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVVCQLGDFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFCFVGKXNHFVFXTHGFTQDGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
	490 500 510 520 530 540
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
	550
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151	CAGTTGGGTC ATGTCGTTCG AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCATC TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCGTAT ACGTTGCCGC
501	CGACCAGGTT GGCATATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCGA TCGCGCCAAT GTCGCCACGC CTTCGGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGA TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCAAA
851	GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAACCTC TTGACCGTTT TTCAGCAATT
951	CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

735

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLTDGAAFA XYGFVAVDGEAAQVAVALFLG					
a501	: : : : : : : : : : : :					
	370	380	390	400	410	420
	VGHVGNQYVAGFDGIHLGSI FNQAY LALTDFLTDGAAFAQDGF FAVDRKAAQVAAAFLLG					
m501.pep	430	440	450	460	470	480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	: : : : : : : : : : :					
	430	440	450	460	470	480
	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDFVGNGEAVAVFFGDID					
m501.pep	490	500	510	520	530	540
	VG YGFTGFCFVGKNHFDVFXTHGFTDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG					
a501	: : : : : : : : : : :					
	490	500	510	520	530	540
	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS					
m501.pep	550	559				
	NKDDLIVXGFGVEGEHHTX					
a501	: : :					
	550					
	DKDDLIVVTGFGIEGEHH					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcctctgac
51  cgtcgccgtc gcttccgcac aggcggggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aacggtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgg
451 ctaccaatac atccgcacgc gttcaaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPIYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNTK ALESSYTLKE DGSSNGIDYV RGNAQTQORR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcctctgac
51  cgtcgccgtc gcttccgcac aggcggggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggcctcttc aaatgggaat acaccaaact t.acaggcaa accatcgtcg
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccggta
451 ccaatacacc cgcacggtc tcaaaggcgg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XKKKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNTK ALESSYTLKE DGSSNGIDYV GNAQTQORRL
151 PIHPHRLQRR QPRRHAA*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

```
g502-1.seq
1  ATGatGAAAc  cgcaCaacct  gttccaaTtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCT
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCGCCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

```
g502-1.pep
1  MMKPHNLFQF  LAVCSLTAVV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKQTQAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFFKTPPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

```
m502-1.seq
1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCGC  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCGCCCCAAA
601 GCGGTGGACG  TGTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

```
m502-1.pep
1  MMKPHNLFQF  LAVCSLTAVV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKQTQAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFFKTPPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTAVVASAQAGAVDALKQFNNDADGISGSFTQTVO	SKKKQTQAHG				
g502-1	MMKPHNLFQFLAVCSLTAVVASAQAGAVDALKQFNNDADGISGSFTQTVO	SKKKQTQAHG				
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180

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```

m503.seq
1   atgtccgcac cgccggcatt ggcaaccatt ttgttccatg cgcgttcgat
51  ttccggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101 ttcttttggc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
1   MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNTF
51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNTFASAAEMRSLR
          |||| ||: ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
g503      MSAPSASVIIIFHAASISASSCSGKGVSKIHWRI SLPTRASSETSTSNTFARAAEMRSFR
          10      20      30      40      50      60

      69
m503.pep  PLCARNAR
          |||||||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
1   ATGTCCGCGC CGCCGGCATT GGCAACCATT TTGTTCATG CCGCTTCGAT
51  TTCGGCATCG AGCTGTTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151 GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTGTGTGTG CGAGGAATGC
201 GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
1   MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNTF
51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNTFASAAEMRSLR
          ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNTFASAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNARX
          |||||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
1   ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTCCTGTG TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAGAGCGC TACGGCAACG
151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTT AGACCGTTGT GTGCAGAGAA
351 TGCGCGGTAG

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1 atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggg gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttc gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa ataccaccaat
451 atcggccctt ccatcgtgta ccgcatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagcgcacc tgccgaaatc cgcaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggcattttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggc tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgacctggt cgccgggtgc gcttttggtc tatctcggct cggatttggt
1101 gggtttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgc aaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcttgcacgc
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1 MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFAWNLK DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKVTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDPAEI REQFM LAEEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLSH MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFFKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1 atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggg gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttc gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa ataccaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgggttt gcaggacag gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggcattttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggc tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcctc ggggttgcag

```

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```

g504      YLGSVLLVLGTVFMFYVPPKKRAWVLFSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
              370      380      390      400      410

m504.pep  DLNHD
           |||||
g504      DLNHD
           420

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

```

a504.seq
1  ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT
51  CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGACCAT CCGCGTGAAC
151 CATCCTTTGA CCTTGACGCG CATCACGATT TATCAGGCGA GTTTTGCCGA
201 CGGCGGTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
301 ATTGGCAAAC ACAAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA
351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GAAAAAAGC CTGAAATCCA
401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAA ATACACCAAT
451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
651 GTTTTGTAAA GATGGGGAAG GCGCGAAACG TCTGGTTGCC GACGCAACCA
701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAA
751 ACGCTGAACA TCTTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGACG
1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
1101 GGTATTGGGT ACGGTATTGA TGTTTATGT GCGCGAAAAA CGGCGGTGGG
1151 TATTGTTTTC AGACGGCAA ATCCGTTTTC CCATGTCTTC GGCCCGCAGC
1201 GAACGGGATT TGCAGAAGGA ATTTCAAAA CACGTCGAGA GTCTGCAACG
1251 GCTCGGCAAG GACTTGAATC ATGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

```

a504.pep
1  ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMMAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETER
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

m504/a504 99.8% identity in 425 aa overlap

```

              10      20      30      40      50      60
m504.pep      ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI
              |||||
a504           ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI
              10      20      30      40      50      60

              70      80      90      100     110     120
m504.pep      YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
              |||||
a504           YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
              70      80      90      100     110     120

              130     140     150     160     170     180
m504.pep      MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ

```

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```

m505.seq (partial)
  1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
 51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101  CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151  TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201  GAACCCCGAC CCCAAACCGG TCAAAGCCGT TTTTGGGAA ACGGCAAAAG
251  GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301  ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351  CAAACACGAA GGGCTGCTAT TCATCAGGCC GCACATCGGC AGCTACGATT
401  TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451  TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501  GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551  AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601  ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651  GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAATTGG CACACGTCAA
701  AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GCGGACAAG
751  GTTTCGATTT GCACATCCGC CCGTCCAAG GGAATTGAA CCGCGACAAA
801  GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATAT GGATACGCCG
851  TTTCCGACG CAtATC...

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

```

m505.pep (partial)
  1  MFRLLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafYLL
 51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDIET
101  MFKAVHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151  KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201  VPSQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251  FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505 ~g) from *N. gonorrhoeae*:

```

m505/g505

      10      20      30      40      50      60
m505.pep MFRLLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafYLLKEDRARIVAN
          |||||
g505      MFRLLQFRLFPPLRTAMHILLTALLKCLSLSLSCSLHTLGNRLGHlafYLLKEDRARIVAN
          |||||

      70      80      90      100     110     120
m505.pep MRQAGLNPDFKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQALDKHEG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g505      MRQAGLNPDQTQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGWEHVQALDKGEG
          70      80      90      100     110     120

      130     140     150     160     170     180
m505.pep LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g505      LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG
          130     140     150     160     170     180

      190     200     210     220     230     240
m505.pep VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYMTLAAXLAHVKGKVTLFF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g505      VKQIIKALRAGEATIILPDHVPSQEGG-GVWADFFGKPAYMTLAAXLAHVKGKVTLFF
          190     200     210     220     230

      250     260     270     280     289
m505.pep CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g505      CCERLPGGQGFVLHIRPVQGEELNGDKAHDAAVFNRNTEYWIRRFPTQYLFMYNRYKTP
          240     250     260     270     280     290

```

747

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCTGTTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCCACCCC AAAACGGTCA AAGCCGTTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCGGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCTACCAG CATACAAGG GTCAAACAAA
551 TCATCAAAGC CCGCGTTTCG GCGGAAGCAA CCATCGTCCT GCCGACCAC
601 GCGCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCC CGTCCAAGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCTATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCILHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDLET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFFLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPOEGG EG VVWDFFGKPA YTMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRAEY W IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHlafYLLKEDRARIVAN
g505        MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHlafYLLKEDRARIVAN
      10      20      30      40      50      60

      70      80      90     100     110     120
m505-1.pep MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDLETMFKAVHGW EHVQQALDKHEG
g505        MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFFRKPEDLETMFKAVHGW EHVQQALDKHEG
      70      80      90     100     110     120

      130     140     150     160     170     180
m505-1.pep LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTSIQG
g505        LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTSIQG
      130     140     150     160     170     180

      190     200     210     220     230     240
m505-1.pep VKQIIKALRSGEATIVLPDHVPSPOEGGEGVVWDFFGKPAYMTTLAAKLAHVKG V KTLFF
g505        VKQIIKALRAGEATII LPDHVPSPOEGG-GVWADFFGKPAYMTTLAAKLAHVKG V KTLFF
      190     200     210     220     230

      250     260     270     280     290     299
m505-1.pep CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRAEY W IRRFPTQYLFMYNRYKMPX
g505        CCERLPGGQGF V LHIRPVQ GELNGDKAHDA AVFNRAEY W IRRFPTQYLFMYNRYKTPX
      240     250     260     270     280     290

```

m505-1/a505 99.7% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHlafYLLKEDRARIVAN
a505        MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCILHTLGNRLGHlafYLLKEDRARIVAN
      10      20      30      40      50      60

      70      80      90     100     110     120

```


749

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCFSF FVGQVFNPLL AAEMEFHPKT
251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
451 GQMGYGAFFG SHRSCSFSQV GQMGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFAKTM DAIIRQDFRY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

```

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51 TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGG TTGATTTTCA AAGGCGGTTC GGCGAatCGg GGTGTTGTCT
201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
251 CCGTCGCGCG GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCAA CGGTAGCGTT
351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTIT ATCTsGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT CGGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
501 CTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
601 GCGGTCTGCG GCGATGATTT TGGCGGCTTC TTCGTGgTC AGGTTTTTAA
651 TGCCTTGTG GGTGCGGAAA TGGAATTTCA CCCAAAAACG CTCGCTGCT
701 TCGTTCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
751 GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCACTG
801 CTTCCGGCAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC AGAGCGCATA
851 TTGGTGCgCG GGTGCGCTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG
901 CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCAGT
951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTC
1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAATATAG ATGCGACTAT
1301 ACGCCAAGAT TTTGCTATT AA

```

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

```

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVC
51 RVAVDFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGGFLH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHLDDVH
201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFFG SHRSCSFSQV GQMGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRAVDFQRRF					
	: : : : : : : : : : : : :					
g506	MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVVIVLAVVPVCRAVDFQRRF					
	10	20	30	40	50	60

751

```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGSTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGCTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCCG
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTGCGCA ACAGCGCGCG CGTTGTTTCT
1351 GGTACAGATG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAAT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVLRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRLDLVH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAF GIELQRKTAD
351 VAFICGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRVVH
451 QMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFEFPVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAADVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVLRVG					
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAADVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRHLDDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHLDDVHRPFRKLAAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHLDDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHLDDVHRPFRKLAAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVG					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVG					
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVG					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVG					
	250	260	270	280	290	300

753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: : : : : : :					
g507	MLLPALQQGGFLSGGGFGLVGVQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : : : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRRLCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : : : : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTCCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTCGGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGAA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTC	CAATTCGGGC
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCATC	GCCATTCCG	CCAATTCGGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTC	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCTGCGC	CGCTGCTTG
401	TCGCGTTTCA	TGCGTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTGTTCTTC
451	CAAACGGGCA	ATCTGTTCGC	GCAACAGGCC	GCGTTTGTG	CCCAATTCGT
501	GCACGCGCTG	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQQGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFALFVL	GNLFGMGKL
51	LLLQRQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: :					
a507	MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLQQGGGLGGGLKLRLQGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
	:			:		
g508	MVAFGVDQGLLLLQQGGGLGGGLKLRLQGLQGLYAGVLLPALFLNLREFFLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLLELGFIGEGKLLLAFLPVEGLLFLKLGDLLPVVFLFLVFEVDGDFG					
	:			:	:	
g508	YGFQQLVELDVLLVVLLELGFIGEGKLLPAFLPVQGLLFEPEGDLLPVVFLFLRVFEVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGKLRFLQTALLLLAAVRGGLLLVFEFGGGFLQGNDDV					
					:	
g508	KPVLAVGFQQGKLRFLQTALLLLAAVRGGLLLVFEFGGGFLQSSDDV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```
a508.seq
1 ATGGTAGCGT TTGGCGTTGA TCAGGGCTCT CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TCGGGCAGCT TGTTTGTGAC GGTTTGTGAC
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGGCAGG
251 CGAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGTG GTTCAAGCTG
301 GGCAATTTCG TGTGGTAGT TTTGTTTTCG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTGCT
501 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```
a508.pep
  1  MVAFGVDQGF  LLLQQGGLGG  GLKLRLGLQ  GLYAGVLFPT  LLNLREFLL
51  YDNIFVQTL  YGFAQLFELD  VLLVVLGLG  IGEGKLLLA  LPIEGLLFKL
101  GNLLLVFL  LVLVDGDFG  KPVLAVG  GKRLRFQTL  LLLAAVRGGL
151  LLVFEFGGGF  LQNGDVV*
```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLYAGVLPPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAFFFKLDVLLVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVFLLLVEFVDGDFG					
a508	YGFAQLFELDVLVLELGFIGEGKLLLAFLPIEGLLFKLGNNLLVFLVLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGLRLRFQTALLLLAAVRGGLLLVFEFGGGFLQGNDDVVX					
a508	KPVLAVGFQQGLRLRFQTTLLLLAAVRGGLLLVFEFGGGFLQGNDDVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

757

```

551  ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601  AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651  TGTCGGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701  TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751  CACGCCGTTG TTGATTTCTG CGTTGACGCT GACTTTGTGG CGGCGCGTTT
801  CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851  CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901  GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951  GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCT ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCTGC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCCGCT CTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCTT CTCTCGTCTG CCGTAAATAT
1401 TGTAATATGA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCCTGC TGCGGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTGCG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVVQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVQCQAFGK QTAAVVDKGT LQFFQIIQKL
101  LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151  VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201  KRIAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251  HAVVDFVDA EFVAARFAGL PQAQQDSVDF AAQPCQVGI GAAAFALRQC
301  ADAAVEAXDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351  QAAFRAAASG FFDLAAAFV VHVFGDVQNL GEQAAGQGX I VGLLFVQLRQ
401  YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451  VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAAARRQ
501  RYNRPQLFFS EHHHDHDTTR QRRCI PAAVQ PPHPLGRNRH RRAAETFRRA
551  YFGRRLRRFG CRRTXPTLPL RV SAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

```

m509/g509
      10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVQACVLEKLGNHIGVFACVLAQVERH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVVQACVLEKLGNHIGVFACVLAQVERH
          10      20      30      40      50      60

      70      80      90     100     110     120
m509.pep  HVKAEHGYGTDEVQCQAFGKQTAAVVDKGT LQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      HVEAEHGHGTDEVQCQAFGKQAAAVVDKGT LQFFQII EKFLGRSIRLEKAEFAAHTQTER
          70      80      90     100     110     120

      130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      ARFAHSARHNVGNGAAVRFAGDFFVRRREGCQCHYVVVDFDAADGKRFVAVKFVEFAAV
          130     140     150     160     170     180

```

759

```

901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCCGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GSCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGCAGCAG AAACCTTTCG CCGCGCATAT
1651 TTTGGTCTGC GGCTGCGCGC GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGCTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQDSDVF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQIG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNV PMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRPQLFXSE HHHHDHRTTRQ RRCIPAAVQP PHLGRNWHR RAAETFRRAY
551 FGRRLRRFGC RXPCFISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

```

m509.pep      10      20      30      40      50      60
MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH
|||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| |
a509          10      20      30      40      50      60
MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFQACVLEKLGNHIGVFACVLAQVERH

m509.pep      70      80      90      100     110     120
HVKAEHGYGTDEVCQTAFGKQTAAVVDKGT LQFFQIIQKLLCRSIRLEKAEFAAHTQTER
||:|||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| |
a509          70      80      90      100     110     120
HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKFLCRSIRLEKAEFAAHTQTER

m509.pep     130     140     150     160     170     180
ARFAHSARHNVGDGA AVGFAGDFVGRFVGQRRYIAVD FDAADGERQFAVEFVEFAAI
|||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| |
a509         130     140     150     160     170     180
ARFAHSARHNVGNGATVGFFGAGGFVGRFVGQRHHIAVD FDAADGERQFAVEFVEFATV

m509.pep     190     200     210     220     230     240
EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ
::|:|||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| |
a509         190     200     210     220     230     240
KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ

m509.pep     250     260     270     280     290     300
GFEKAHREDGHAVVDFVDAEFVAARFAGLPQAQDSDVF AAQPCQRVGIGAAAFALRQQC
||:|||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| | |||||:|:| |
a509         250     260     270     280     290     300
GFKAHRKDGHAVVDFVDAEFVAARFAGLPQAQDSDVF AAQPCQRVGIGTAFALRQQR

m509.pep     310     320     330     340     350     360

```

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRT	PQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRS	WTTLSAAIMT	
g510	MPSRT	PQKRGYSCPKRDSA	FWQALSISVILRAKSPIAKS	PPFREVFNRS	WTTLSAAIMT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVXDFXVDL	FDVHPLILIAA	
g510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVHDFD	VDLFDVHPLILIAA	
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAGG	GGTTATTCCT	GCGCCAAGCG
51	GGATAGTGCT	TTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CGCCGTTCA	GGGAGGTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCCAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATCCGACTG
251	CCTGCAACAG	TGTGTCTTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTC	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTGCCG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRT	PQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR	
101	XVHDFD	VDLFDVHPLILIAA	FPAVGGGALP	VR*		

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRT	PQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRS	WTTLSAAIMT	
a510	MPSRT	PQKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRS	WTTLSAAIMT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVXDFXVDL	FDVHPLILIAA	
a510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRXVHDFD	VDLFDVHPLILIAA	
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACCAGT TTTGCCAAGC CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTGGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCGCTG
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATCTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTGAGGCC TCGCTGGCA CGCGTTACCG
551 CCAAATTGCG CGGCGGCGTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMF RFEAQTMNF EGRKKGTLQI FRQTKVEEAA
151 QDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVVPYRRLKPEECAEFEPALARVTAK
a512                                |||
                                130      140      150      160      170      180
                                TGMNFEGRKKGTLQIFRQTKVEEAAQDIAVLERYGVVPYRRLKPEECAEFEPALARVTAK

                                40      50      60      70      80      90
m512.pep                                IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
a512                                |||
                                190      200      210      220      230      240
                                IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQTISRIDHNGLRIKTVETKQGGLK

                                100      110      120
m512.pep                                QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
a512                                |||
                                250      260      270
                                QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCGTTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```


765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCGAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTGTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTCG CGATACCSTC AAAGCGGCGT
551 GGGGTGCGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCTCG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAGTCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTT CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCGT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTG ATACCATCAT
951 CGTTTGTCTT TGCACGCGCT TCATCATCTT GATTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 .AAATGGGCA AAGACCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG FVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101  VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151  WLGVLFALSL IFCFGVFVEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201  PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNPIM PDVFGQIFSG
251  AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301  VSQGMQMLG VFDVTLIVCS CTAFIILYQ QPYGDLSGAA LTQAAIVSQV
351  GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401  WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451  KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||

a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
m513.pep
TIIVCSCTAFIILYQ QPYGDLSGAALTQAAIVSQVQWGAGFLAVILFMFAFSTVIGNY
|||||

a513
320 330 340 350 360 370
TIIVCSCTAFIILYQ QPYGDLSGAALTQAAIVSQVQWGAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL
|||||

a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL

160 170 180 190
m513.pep
LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
|||||

```

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVDGGFDG VLQGFGEVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||
g515      AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAAACRDAIAAESAQSAAGGGLTDGFGAVHIRMAA
|||  |||||  |||  :  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515      VERAAGECADEVSDQPARNGGIEEDGVAAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                90      100     110     120     130     140

                                100     110     120     130     140     150
m515.pep      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
|||  |||||  |||  :  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515      GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLSGLHRRAFGVFDAAVR
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep      VQGGFLFALFCQADGGXRIQIPFVVKVGVAADVCHQTGIGKSGATVFGGVAGDVGDFG
||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515      VQRCFLFALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep      LQGFGEVVGSTGAFAFADVNGNVQRLVLELDLXDXAQPHADALSQXFAEIGFGGGCA
||  :|||  :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515      AQGLFGEVGGAGAFAFADVNGNVQRFVLELDLDFDAQAHADALSERFAEVFGGGRAR
                                270     280     290     300     310     320

                                280     290     300
m515.pep      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515      CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
                                330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GGCGTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAPACCGTA GGTGTTGCCG

```

q515-1.pep

m515-1.seq

m515-1.pgp

m515-1/q515-1 91.7% identity in 312 aa overlap

g515-1.pep MVQIQVVRAGVARGLHSEFARAVTAEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDV
|||||
m515-1 MVQIQVVRAGVARGLHTEFARAVTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV
|||||

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep  GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKGVADVLRHQ
              |||||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKGVADVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep  LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
              |||||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
              250     260     270     280     290     300

              310
a515-1.pep  DFAQPHADALSQX
              |||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1  atgttggtcc gtaaaacgac cgccgccggt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcaccgg caaacacggt gacaaagacc aaatccggcg cttcgggtgtg
151 gttgccgaag acaatgcccc attggaaaag ggcagcctgg tgatgatggg
201 cgggaaaatac tgggttcggcg tcaatcccgga agattcggcg aagctgacgg
251 gccttttgaa ggccggggtg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg ccgcccacca agccctgccg gtcaaattcg aagcggccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggcctaaa
451 ctcgacaatc ggaccattta cagcgctgac gtatccggca aagcgaataa
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatgt
551 tgcccggcga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccggg gtgctggtct tgcctatggc tetgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT POKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1  ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCAG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCT TCAATCCCGA AGATTCCGGC AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAATAA

```

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```

1  MLFRKTTAAV LAATLM1GC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDVAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV1DKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV1DKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60
              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDT1PSYARHQALPVKLESPGSQN
              70      80      90      100     110     120
a516           GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKQFQMVPEPN1PRFA-YQALPVKLESPASQN
              70      80      90      100     110
              130     140     150     160     170     180
m516.pep      FSTEGLCLRYDTPDKPADI1AKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              130     140     150     160     170
a516           FSTEGLCLRYDTPDRPADI1AKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
              120     130     140     150     160     170
              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAV1LALPAAALGAVVDAARKX
              190     200     210     220     230
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDVAV1AVLALPVAALIAATNSSDKX
              180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatacggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatgaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggtcg atttggtctg
201 tgcgcgccgt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgcgtt agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggttag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA QEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGLIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCAGATT TGATGTTTTT GGGCAGGTGCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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```

              70      80      90      100      110      120
          130      140      150      160
m517.pep  FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX
          ||||| ||:|||||:|||||:|||||:|||||: ||
a517      FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVVGQKTOFLAGFDGRPHX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac catTTTTTca gcataaatat tctgaccoga
151 agagcggcat ctccacgggc aaccgtgttc agactgcata aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcggcaaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg g.jgagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTC AGACGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPQATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
          ||||| ||:|||||:|||||:|||||:|||||: ||
g518      MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
          10      20      30      40      50      60

              70      80      90      100      110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRCAVILSN
          | ||| || : ||:| ||||| ||| |||||
g518      RLHQAVRFHKMPKTISKMRNRYAVRITPPRAATLHYNRLPL-----
          70      80      90      100

          120      130
m518.pep  GRKSDPAFVAESEI
          ||||| |||||
g518      --KKSDPAFVAESEI
          110

```

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```

101 SNYIMAITQL AQTTLSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQOS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFAK LAKEDNTRIK PAKVAEIGNP
301 NFRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
1   ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTGCGT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCGCCCAA TGTGCGCGAC ATCGGCAGCC
551 TGATTCTGCG CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
1   ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTGGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519

m519.pep                                10      20      30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLSVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100     110     120     130     140

m519.pep                                40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
g519      GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
          150     160     170     180     190     200

m519.pep                                100     110     120     130     140     150
IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
|||||
g519      IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
          210     220     230     240     250     260

m519.pep                                160     170     180     190     200
NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL- ISAGMKIIDSSKTAK
|||||
g519      NLKIAGQYVTAFAKNLAKEDNTRIKPAKVAEIGNPNFRHEKFSP EAKTAK
          270     280     290     300     310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
1   ATGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT

```

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAAYRHS KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLYRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGCGGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGGCGGCCGG GCGTTGGGGT
 451 GTGAAGGTTT TGGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAAAATCG CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAAYRHS KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLYRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					


```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctgggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa ggcggggcga cgggccgatt
401 ttggcgggct tttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa ggcgcgggaa atttctctct cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaaacct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGGR RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTTCGT TGCCGTATTC GGCAGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTGG

```

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLLKCKYX					
a520	CLLASLCLLVSRLLKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCGGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GGCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCCGCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGTCG GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTTACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCCGCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

a521n.pep

1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROONI QALQRELGRM *

m521.seq

```

1   ATGAAATCAA  AACTCCTCTT  AATCCTAATC  AACTTTTCCC  TGATTTCAAG
51  CCCATTGGGT  GCGAATGCGG  CCAAAATCTA  sACCTGCACA  ATCAACGGAG
101 AAACCGTTTA  CACCAsCAAG  CCGTCCAAAA  GCTGCCACTC  AACCGATTTG
151 CCCCCAATCG  GCAACTACAG  CAGCGAACGC  TATATCCCGC  CCCCAAACGCC
201 CGAACCGGTA  TCATCACCGT  CAAAGCGCGG  ACwGGTTGTc  AAGATATAAG
251 CCCCGGTCAA  AACAGTATCC  AAGCGGCAA  AACTCAsTAC  GCGCCGCGCG
301 CAACAAGCAC  CCTCAAACAA  CAGCAGACGC  TCCATTCTCG  AAACAGAATT
351 GAGCAACGAA  CGCAAAGCAT  TGGTTGAAGC  CCAAAAAATG  TTATCACAAG
401 CACGTCTGGC  AATGGGCGGC  AACATCAACC  ATCAAGAAAT  AAATGCATTA
451 CAAAGCAATG  TATTGGACAG  GCAGCAAAAT  ATTCAAGCCC  TGCAAAGGGA
501 ACTGGGCGCT  ATGTAA

```

m521.pep

```

1  MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51  PPIGNYSSER YIPPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROON IOALORELGR M*

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m521/q521

	10	20	30	40	50	60
m521.pep	MKS K L L L I L I N F S L I S S P L G A N A A K I X T C T I N G E T V Y T X K P S K S C H S T D L P P I G N Y S S E R					
	: : :					
g521	M K S K L P L I L I N L S L I S S P L G A N A A K I Y T C T I N G E T V Y T T K P S K S C H S T D L P P I G N Y S S E R					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	Y I P P Q T P E P V S S P S N G G X V V K Y K A P V K T V S K P A K S X T P P P Q Q A P S N N S R R S I L E T E L S N E					
	: : : :					
g521	Y I L P Q T P E P A P S P S N G G Q A V K Y K A P V K T V S K P A K S N T P P - Q Q A P V N N S R R S I L E A E L S N E					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	R K A L V E A Q K M L S Q A R L A K G G N I N H Q E I N A L Q S N V L D R Q Q N I Q A L Q R E L G R M X					
	: : : :					
g521	R K A L T E A Q K M L S Q A R L A K G G N I N H Q I N A L X S N V L D R Q Q N I Q A L Q R E L G R M X					
	120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQP
 101 LDRLSEKQIR SFGKLGAEQ LDLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: : :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
 201 GTTGGCCGAA AAATGGCAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQP
 101 LDRLSEKQIS SFGKLGAEQ LDLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
a522	SCVKNIPFAEKWQNDLRARGLDNNTRLTVDYCKMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

789

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1  ATGACTGTAT GGTGTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTGTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

```

              10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF
              |||||
a523           MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF
              10      20      30      40      50      60

              60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFVRGTHWQAQNTGQEELEPGTRA
              |||||
a523           VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFVRGTHWQAQNTGQEELEPGTRA
              70      80      90      100     110     120

              120
m523.pep      LIVRKEGNLLIIITHPX
              |||||
a523           LIVRKEGNLLIIAKPX
              130
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1  atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51  agcggcggtt gccgaaatgg ttcaaatcga agcgggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcgggtt caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccgg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactgggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

791

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
  51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
 101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRT
 151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
a525      MKFTRLLEFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90     100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRLQLPHYSRLVCRRTTERPARCRXKAARTTGA
a525      AQGKRLPTIDWEFAGLASATQXKRLKRLQLPHYSRLVCGWRPERPARCRQXVARTTGA
      130     140     150     160     170     180

m525.pep  FMICTGX
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
  51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
 151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
 201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
 251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
 301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTT CCGCCAACGC
 351 CTATTGCGCC GCACAAGGCA AAGCCTGCC GACCATCGAC GAATGGGAAT
 401 TTGCCGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
 451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
 501 GCACGATGTC GGCAAAAGACC GCCCGAATA CTGGGTGTT TATGATATGC
 551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
 601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCAT CTGTCGGGGC
 651 GAGCGACTCG TCCAACATG CCGCCTTCT CCGCTACGGC ATCCGCACCA
 701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCG CTGCGCAAGC
 751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
  51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
 101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
 151 YNRITLDWYA DGGRKGLHDV GKDRPNYWG VYDMHGLIEWE TEDFNSSLLS
 201 SGNANQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNGLGRCAS
 251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
  51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TCKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLSS
201 SGNANAQMF C SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
a525-1	MKFTRLRLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSPSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG					
a525-1	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
a525-1	YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1	LHNLGFRCTSRX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcggctgcg
51  gcttggtcgg tctgcccgcg ggaatggcgg aagtgatcgc gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtctctctc
151 atacagaagc cgcgcctcgg gtgcccggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggtttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgcccacca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPSVFFQP VLAAVALGR SAVGMGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51  GCTTGGTGCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

795

	70	80	90	100	110	120
m527.pep	ALVVQTFN	DFIGKXNXASVXXIAD	VYGF	TVFDLR	AVYLNPTQ	FDVLLRKGTGLEKTCRP
a527	ALVVQTFN	LDFIGKIERQVDNIAD	VYGF	TVFDLR	AVYLNPTQ	FDVLLRKGTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 cgggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacqaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgttttgaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGGA
351 CTGCTTGGA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFACGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

797

```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAG AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:
m528-1      KQGLRRNGLSERVRWX
          130

```

799

```

|||||
m529 MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
g529.ppep GSGAVRASDLEKRRTPAVQQPADAGSIEKRQRRPLRAATAANAWLVVDGKSPAEISAAFX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529 GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLER-DGSQRWLVVDGKSPAEIWPLLK
      70      80      90      100     110
m529 AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529.seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTCGAAGTCC CACCTGATTT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGTGTCGC GCCTCGAGCG CGACGGCGAGC
301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CATGTCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGGCGCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGCGCT TTCCGACATC TTCTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTGCGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTGCGCA ACGGCTCGCG CATCGTCTCTG
1051 CTAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529.ppep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLSV KGVRLERDGS
101 QRWLVVDGKS HAEIWPLLKA FWQENGFDIK SEEPaIGOME TEWAENRAKI
151 PQDSLRLRLFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDQTTV WQSPSPDPNL EAAFLTRFMQ YLGVGQQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRALAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

m529/a529 99.2% identity in 375 aa overlap

```

      10      20      30      40      50      60
m529.ppep MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
|||||
a529 MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
      10      20      30      40      50      60
      70      80      90      100     110     120
m529.ppep GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVVDGKSPAEIWPLLKA
|||||
a529 GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVVDGKSHAEIWPLLKA
      70      80      90      100     110     120
      130     140     150     160     170     180

```

g530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRAGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRICPGRIPPISVRRGWVRRTWCKSESQVR	99
	:	
g530	ERAAGARAVRIRPRRIPPISVRRDWVRRTWCKSESAGR	99

```
a530.seq
1   ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
51  CTGTGTGA TG GATATTAAAG TGTTTGTGTC GTTATGCCGT CCGAACGTT
101 CGGACGGCA T GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGGCG
151 GGACTTTTGC CTGTCCGCCCT TCCGTAGCGG GAACAGCGCG CAGCGCGGAC
201 TGCGGTTCC G ATCTGCCCAT GCGCGATACC GCCCATTTCC GTGCGCGGGG
251 GCTGGGTTCG CAGAACATGG TGTCTGTAAT CGGAATCAGC CGGTCTGTGA
```

a530.pep

```
1  MSASAAMTGL IWVIIVSSCVM DIKVFVALCR PNGSDGMAIF KVLRLSGRR
51 GLLPVLRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*
```

```

      10          20          30          40          50          60
m530.pep XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXI FKVVLR LSGRGL LXVRFP SA
         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | : |||
a530     MSASAAMTGLIWVIVSSCVM DIKFVALCRPNGSDGMAI FKVVLR LSGRGL LPVRLP SA
      10          20          30          40          50          60

      70          80          90         100
m530.pep ERAAGGRAVRICPGRI PPISVRRGWVRRTWCRKSESVGRX
         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a530     ERAAGGRAVRICPGRI PPISVRRGWVRRTWCRKSESAGR X
      70          80          90         100

```

```
g531.seq
  1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCCG  CTGGCATTG  ATGTTTGCCG
101 GAACATGGCT  GCTTGCCTAT  GCCGGCGGCT  ATCAAATCTA  CGGCGCAGGC
151 ATCTTGTGGA  CGGTCCGACT  CATCAGCCTT  GCGCGCATAC  TGCGGACTA
201 TATGGCAGGC  ATGTTGGGGG  TAAATAACAC  TGGGGCAGCG  AAATCGCCG
251 TCCGAGGTGC  ATTGCCGGGC  AGCATCATCG  GCATATTTTT  CTCCTTCCC
301 GGACTAATAC  TCGGCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
351 TCGCGCAAT  ATGCTTCAGG  CAGGTAAAGC  GGGCTTGGGT  ACGCTGTTGG
401 GGCTTGTCTG  CGGCACGGCG  TTCAAAATCG  CTGCGCGGCT  ATCCATCTTG
451 TTTATCCTGT  TGGTGAAATA  CCGCATAC  CTGTTTAA
```

```
g531.pep
  1  MTALLVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51  ILWTVGLISL GGILADYMAG MLGVKYTAG KLAVRGALAG SIIGIFSLP
101 GLILGPFFIGA AAGELIDRRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF
```

```
m531.seq
1  ATGACCGTAC  TGACCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCGGGCATC  GTTTaCCCCG  CCCTGCCCGG  ATTGGCATTG  ATGCTTTGCCG
101 GAACATGGCT  GCTTGCCCTAT  GCGCGCGGCT  ACCAAATCTA  CGTGTGCGGC
151 GTTTTGTGGA  CGGTGGACT   CATCAGCCTT  GCCGGCATAc  TGGCGGACTA
201 TGTGGCAGCG  ATATGGGGGA  CAAATATAC   CGGAGCGGGC  AAGCTCGCCG
251 TTCGCGCGC  ATTGGCCGGC  AGCATCATCG  GCATATTTT  CTCCCTTCCC
301 GGACTAATAC  TCGGTCCCTT  TATCGGCGCG  GCGGCAGCG  AACTGATCGA
```

803

```

|||||
a531      AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
              70      80      90      100      110      120

              130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
|||||
a531      MLQAGKAGLGTLLGLIVGTAFAKIGCAVSILFILLVKYIAYLFX
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgcgt gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgatctcgg tgctcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCCGCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTGCTT
301 ACCGTGATGA TTGCGCTGGG CCGGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATCGCATG ATTTGACGC TCTTGGGCGT ATCGTTTGTC GGCGCGTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGCGATT ACCGATTTCG GCGGCGGCTT CCGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATG TGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGCGGCT CCGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTTGGCTGA CGGCTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTACGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTG
1051 GTGCTGTGTT GTCTGTTCCC CGTTGTCGGT CCGCGGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTGCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTGTT AAAAACCCTG CCGTCTGTG CCAAACTCT ATTCCGCGC
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGYLQVN RFGVPVSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVVL IGLSLVHVGITDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGFMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

```

      10      20      30      40      50      60
m532.pep MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532      MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
      10      20      30      40      50      60

      70      80      90     100     110     120
m532.pep AYLVSAMVASGVGTYLQVNRFGPVGSGMLSISQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532      AYLVSAMVASGVGTYLQVNRFGPVGSGMLSISQSVNFSFVTVMIALGAGMKEGGLTKDAM
      70      80      90     100     110     120

      130     140     150     160     170     180
m532.pep ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVVLIGLSLVHVGITDFGGGFGAK
a532      ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVVLIGLSLVHVGITDFGGGFGAK
      130     140     150     160     170     180

      190     200     210     220     230     240
m532.pep ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
a532      ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAVGLIAGYIVALFLGKVDFSALQ
      190     200     210     220     230     240

      250     260     270     280     290     300
m532.pep NLPLVTLVPVPFKYGFAFDWHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL
a532      NLPLVTLVPVPFKYGFAFDWHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL
      250     260     270     280     290     300

      310     320     330     340     350     360
m532.pep RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRRHVHVGKYIAVILVLLGLFPVVG
a532      RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRRHVHVGKYIAVILVLLGLFPVVG
      310     320     330     340     350     360

      370     380     390     400     410     420
m532.pep RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
a532      RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF
      370     380     390     400     410     420

      430     440     450     460
m532.pep KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532      KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
      430     440     450     460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1 atgccctttc ccgttttcag acaantattt gcttngtcc tgetacggtt
51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcggttttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRRHGDVEAFA						
	:						
g535	FVPLYGGLARVAVAVEGGFFDQGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
		130	140	150	160	170	180
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFOAFGGVDGHELDGLFACAC						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHHQLDGGFACPC						
		190	200	210	220	230	240
	240	250	260				
m535.pep	LVFTGFEGGIIAXEGENGEGGVV						
g535	LVFAGFEGGVAAQEGEDGEGGIV						
		250	260				

```

a535.seq (partial)
1   TTCAGACGGC CTTTTCGCTT GTCCTTGCTA CAGTTTTTTG CCATAGGTCG
51  GATTCTCGAA TCCGACATT  CCAACAGCGG TTTTTCGGAA ACGTAGAGAC
101 CGTCAAATAT TTTTGTCCGA TACGAGTATC CAGCCTCGAT TTTCAAATTTA
151 CATCGCTTCC AATTTTCGAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTTAC TGGCGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGCTTT GTCCGATACG
301 GAAACCTGCG TAGTTTGGG  GCTGTTTGTA GTGTCGATG ATTTTGTCTT
351 TGGGCGCGGC GGGTTTGGCG CTTTGTCCAT AGCGGTCGTA GGCGGGTTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTCTTT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATGCGT TGTTCGCCCA
501 TGGTGATGTA GAGGCGTTTG CGGCGCGCGG TGATGCCGAC GTACATCAGG
551 CGCGCTTCTT CTTCGAGGCC GCGCGGTTTC GCAAGGCTCA TTTCTGCTGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTTCAAAG
651 CTTTGGCGGC GTGCACGGTC ATGAGTTGTA CGGCTTTTTT GCCCGCGCCT
701 GCTTGGTTTT CGCCGGAATC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGACG GGGTCGTCG A

```

```

a535.pep (partial)
1 FRRPFALLSL QFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
51 HRFQVRLKLG QLFHALFAEI DGQSGGFAFI CGIDNHAGAE FGVADVLSDT
101 ETCVGLGLFV VVDDFVFGRG GLARVAIAV VGGFDGQVVQ YFGRDFFDEA
151 GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEEA AAFGKAHFAG
201 EAAFFHVAGE YGVKFQAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251 GEGGV*

```

```

m535.pep      10      20      30      40      50      60
               MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEYPTYISNLHLFQF
               |||||::|:|||||:|||||:|||||:|||||:|||||:|||||
a535          FRPPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF
               10      20      30      40      50

m535.pep      70      80      90      100     110     120
               RKLGVQLFHALFAEIDGQSGGFATICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a535          RKLGVQLFHALFAEIDGQSGGFATICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
               60      70      80      90      100     110

m535.pep      130     140     150     160     170     180
               IFGCGGLARVAIVTVVGRLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG
               :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a535          VFGRGGLARVAIAVVGGFDDGQVVQYFGRDFDEAGDDAELGLSVQHALLRHGDVEAFAG
               120     130     140     150     160     170

```

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

```

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

```

m537.pep (partial)
  1 MKSLFIRLLL LGSAAGVFIH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAIQIGLHK LAHAPVLENS ARRHASVLTN NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE SGAA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

```

m537/g537

      10      20      30      40      50      60
m537.pep MKSLFIRLLL LGSAAGVFIHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIAIQIGLHK
||||| ||||||| ||||||| ||||||| ||||||| |||||||
g537      MKSLFIWLLL LGSAAGVFIHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIQTQIGLHA
      10      20      30      40      50      60

      70      80      90     100     110     120
m537.pep LAHAPVLENSARRHASVLTNPNEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
||||| ||||||| ||||||| ||||||| ||||||| |||||||
g537      LAHAPVLENSARRHARYLTNPNEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
      70      80      90     100     110     120

      130     140     150     160
m537.pep TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
||||| ||||||| ||||||| |||||||
g537      TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
      130     140     150     160     170     180

g537      GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE
      190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

```

a537.seq
  1 ATGAAATCCC TTTTATTCG GCTGCTCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGCG CCCAAATCGG TTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAATTCG GCCCGCAGGC ACGCACGCTA TCTCAGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGTGG
501 CGAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
601 TACCGCAACG CCGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGCGGCAC
701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
801 GATGAAAAGT TTCAAGCTGT ATCAGGTGTA AAACGAAATC CGCCCCGTCA
851 GGGTTTTTAA CGCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACCGC
951 GGTATTTCGAT TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
1001 TTAGAACCCG AAAACCCGAT TACCTTATT TTGAGGTAAA CGGCGGCGAG
1051 AACTTGGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
1101 CTGGTGTTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGCCA

```

q538 . pep

1	MSGRTGRNSA	TQAQPERVML	VGVLMDKDDT	GSNAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	TELKQKDRPH	TALFVGTGKA	AELSEAVAGD	GIDLVVFNHE
101	LTPTQERNLE	KILQCRVLDR	VLGLAIFAR	RARTOQGRDQ	VELAQQLSLHA
151	GLRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLTAHRINA	LKQQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDQLFATLD
251	TTARRLYISP	ACSIILTDTV	GFVSDLPHKL	ISAFSATLEE	TVQADVLLHV
301	VDAAAARNSGQ	QIEDVENVLQ	EIHADHPICI	KVYNKTDLLP	SEBQNTGIWR
351	DAAGKIAA VR	ISVAENTGID	ALREAIAYEC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTAGTG
101	CCGCCCTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGG	CGGGCGGCGA	TTCCGTGCGC	TGGGAGACTG	CCAAACCGCA
201	CGGTCCGACC	ACCCGCGTGT	TTGTGCGCAC	GGGCAAGGCG	CGGGAGCTGT
251	CAGAAGCAGT	TGCCGCAGAC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCACGCCCA	CGCAGGAAGC	TAACCTTGAA	AAAGAAGCTA	AATGCCCGGT
351	ATTGGACAGG	GTAGGCGTCA	TTCTGGCGAT	TTTCGCTCGC	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CGCAATTGAG	CATTATGGCG
451	GGACGCTTCA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	CGCGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAACT	GGAACCGCAC	CGCCGATTGA
551	TCGCCCATCG	GATCAATGCC	TTGATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCnCGCGAA	TCGGGACCAA	TCAAACCGTT
651	TGCGCTGCTG	GGCTATACAA	ATGTCGCGAA	ATCAGCCCTG	TTCAACCGGC
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCCTGA	CCGATACCGT	CGGATTGCTn	AGGCATCTCG	CGCAcAAACT
801	GATTTCCGCC	TTTTTCgC .A	CGCTGGAAGA	AACCGCGCAA	GCCGATGTGC
851	TGCTGTCAGT	GCTGATGCTG	CGCGCTCCGA	CACAGCGGACA	CGAGATTGAA
901	CACGTGAAAA	ACGTACTGCA	AGAAATCCAT	GCCGGCGATA	TTCCGTGCAT
951	cAAGGTGTAC	AACAAAACCG	ACCTGCTGCC	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CCGCCCTCCG	CATTTCCGTT
1051	GCTGAAAAAT	CCGGTATAGA	CGCACTGCGC	GAAAGcATTG	CCGAGTCTTG
1101	TGCCGCGCGA	CAAAACACAG	ACGAACCGGA	AATGCCATGA	

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538 . per

1	MTGRTGGNGS	TQAQPERVML	VGVMLDKDG	GSSAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLVVFNHE
101	LTPQOERNLE	KELKRCVLDR	VGILILAI FAR	RARTOEGRLO	VELAQLSHLA
151	GLTRIGYGH	LQSQRGIGMK	GPGETKLEFDR	RLRIAHRRNA	LILQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILDTVG	FDLPHKLISA	FSXTLEETAQ	ADVLHVVD	AAPNSSGQIE
301	DVENVLQEI	HAGDIPCIKV	NKTDLLPSEE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EAIAESCAAA	PKTDTEMP*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng)

from *N. gonorrhoeae*:

m538/q538

[illegible]

813

201 ORALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILDTV GFVSDLPHKL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538.pep	70	80	90	100	110	120
	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLDR					
	70	80	90	100	110	120
m538.pep	130	140	150	160	170	180
	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	190	200	210	220	230	240
	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	250	260	270	280		
	AKDKL-----SPECSIILDTVGFVSDLPHKLISAFSXTLEETAQADVLLHV					
	:					
a538	AKDQLFATLDTTARRLYISPECSIILDTVGFVSDLPHKLISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538.pep	290	300	310	320	330	340
	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	350	360	370	380		
	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

1	atggaggatc	tgcaggaaat	cgggttcgat	gtcgccgccg	taaaggtagg
51	tcggcagcgc	gaacatcatc	gtctgcatca	tacccagtc	ggcaacggca
101	aggcggacga	tgtattgttt	gcgttccttt	tggttggcgg	cttcgatttt
151	ttgcgcgtca	tagggtgcgg	cgggtgtagc	tgtctgccgg	attttcaaca
201	gaatgtcggg	gaggcggatt	ttgccgtcgt	cccagacgac	gcggcagcgg
251	tgcgtgctgt	aattgaggtc	gatgcggacg	atgccgtctg	tgcgcaaaag
301	ctgctgttcg	atcagccaga	cgcaggcggc	gcaggtaatg	ccgctgagca
351	tcagcactgc	ttcgtgcgtg	ccattatggg	ttccacaaa	gtcggattgg
401	acttcgggca	ggtcgtacag	gcggatttgg	tcgaggattt	cttcggggcgg
451	cagttcgggt	tttttcgcgt	cggcgggtcg	tcgtttgtaa	taactgcccc
501	agccggaatc	gatgatgctt	tgtgcgactg	cctgacagcc	gacgcagcag
551	gtttcgcggg	cttcgccttc	gtagcggacg	gtcagatgca	ggttttcggg
601	aacgtccagc	ccgcagtggg	aacagggttt	tttcatggca	tttcgggtttc

815

	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539.pep	130	140	150	160	170	180
	LARAAGVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539.pep	190	200	210	220	230	240
	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVGNVQPAVETGFFHGISVSSVFGAAQVSAMASRSASIPVFS					
	190	200	210	220	230	240
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSSTFSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSSTFSTSSICCPFLRA					
	250	260	270	280	290	300
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGCTGCGG CCGGTGAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTCT ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTCGCGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTTCATGGC TTTTCGGTTT
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CCGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIFD VAAVKVGRQR EHHRLHHFQP GNGEADDVLF AFFLVGGFDF

```

```
m540.seq (partial)
1 ..CCGAACCCGA TGCCGCTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTGTG
51 CCACCCGGAT GGGGGCAGTG TCGTATTGTG TCGATTCTGC CCGGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTGTC TGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
201 TTTTCAGTTT GCTGATTTC AATCATGCGC CGTGCCCGCC GCCTTTGCGC
251 CAGTTGAAAT CCAATATAC CACATCATG TAAGCGCGGG CGGC GCGGTG
301 TCCGCAAGTC TTGATTTCGC CCATATTTT CCAGCGTGA
```

```
m540.pep      (partial)
1      .PNPMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
51     GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
101    SAVVDLRHIF PA*
```

m540/g540

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                               |||||
g540                          GNGVFYQNGKLANAVSACRLPNRQTFFVPVPPNMPMPSEPSDGIGCLFVHSDGGRFVLCRFV
                              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep          AVIQHAEFDGDSALXFavgigIPIQGIGTTAIFLLVEVFTFADFNHARAAAAAFAPVEIPIH
                  |||||:::|||||:|||||:::|||||:::|||||:::|||||:::||
g540              AVIQHAEFDGDasLRFAVGvgIAQGIRAAAvFLLEVFafADFNHTRAAAAfAPVEvPIG
                   70      80      90      100     110     120

                        100      110
m540.pep          HIIVRRGGAVSAVVDLRHIFPAX
                  |||||:::|||||
g540              HIIVRRGGTVSAVVDLRHIFPAX
                   130      140

```

```
a540.seq
1  ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC
51  TGCCAATGCG GTTTCGGATT GCAGATTGCC AAACCGGCCA ACCTTTCCCG
101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTACAGACG CATCGGGTGT
151 TTATTGTGTC ACCCGGATGG GTGCAGGTTC GTATTGTGTC GATTCGTGCG
201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG
251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCTGCTG
301 GTAGAAGTTT TCACGTTTGC TGATTTCATC CATACGCGCG CTGCCGCCGC
351 CTTTGCGCCA GTTGAATACC CAATACACCA CATCATCGTA AGCGCGGCG
401 GCGCGGCGCG CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A
```

a540.pep (partial)

```
1  MPSSRRNGV FYQNGLANA VSDCLRLNQR TFPVMPNPM PSEPSDGIGC
51  LRVHPDGRF VLGRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
101 VETTFADFN HTRAAAFAP VEIPIHHIIV RRGAAAAAVV NLVHVEP
```

819

```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCCG
101 CATTCAAGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATA1CCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC SVLSLMFSVS ASRLT*CAPE ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
|||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
|||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc gggtatttgc cgcggttttt ggctttcaac tcggcaatca
51  gcccgctgat gccttttggt ttgatgattt cgcgcaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
151 gccgccgctt tggtaggtgg taaagtccat attgacgggc tcttgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgctt
351 gtttttgccg gtccggacgg gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggcaca accctgtgtg
501 cgcttttgcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggtttttccg taccgcccgc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcccga gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaaccgccga tgtcgccgaa atcggcataa
1001 acggcgtaag ttttgtccga accgccgaac ccgcgcgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcgcgc gatcaagacg aacagtcgga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF GFOLGNQPV DAFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

821

```

m543.pep  VGRGAPRVADRQCGHT1 EIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      VGRGT130PRVADRQCGHTLEIEIGNRIGFGFWACRSRVA140AFEDGQNL150CGVLADLSHC160VGRRG170
          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA190AVGIFLGKTRHEFADK200V
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIA210ALSVFLGEAGHEFTDQV220
          190      200      210      220      230
m543.pep  FQNHCR240TGYDGVAGSKVFRVAALLOPDVLLAQKSR250SQDLRGNVAAELILAVOIEAHPRL260
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      FQNHCR240TGYDGVAGSKVFRIAALLOPDVLLAQKSR250SQDLRGNVTAEILILAVOIKAHPR260L
          240      250      260      270      280      290
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQ300TADVAEIGINGVSVFRTAERRTAGHAESEKGNR310
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      IGFRVKPDSADAPDQYACGFDGGIDLQ300TADVAEIGINGVSVFRTAERRAARHAESEKGNR310
          300      310      320      330      340      350
m543.pep  RRANQDEQSDPKFQYVLLHX360
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      RRADQDEQSDPKFQYVLFHX360
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTT251TAAAT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTG GCCAACGCTT
351 GTTTT351TGCGC GTCGGACGCG GTGCGCCAAG GGTGCGCAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTT501TGACG GATTGGTTT ACCCGCTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTT551
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTT651TCCGC ATTGCCGCCG TCGGCATTT TCTCGGCAAA ACTCGTCATG
701 AATT701TGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTA801CTGCTC GCCCAAAGT CCCGAAGTCA GGATT801TGCGC GGAAACGTCG
851 CTGCTGA851ACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATT901TGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCC901TG
951 CGGATT951TGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAA1001ACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCG1051GAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLA1AVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALV51GGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGAD101QQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVG151ITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*201FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCR201TGYGD
251 GVAGSK251VFRV AALLQPDVLL AQKSR251SQDLR GNVA251AELILA VQIEAHPRLI
301 GFRVKSD301SAD APDQYACGFD GGIDLQ301TADV AEIGINGVSF VRTAERRTAG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

1	ATGAWAAAAA	TACTCACCGC	CGCCGTCGTC	GCACCTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CGGACCTGCA	CGGAAAAACG	GTTTCCAACG	CCGACCTGCA	AGGCAAAAT
151	ACCCTGATTA	ATTTTGGTT	TCCCTCCTGT	CCGGGTTGTC	TGAGCGAWAT
201	GCCCAAAATC	ATTAACACGG	CAAAATGACTA	TAAAAWCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCCTTATCG
401	GCAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCCCAAC	CGATTTCCGG
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCGCAATAG	

MS44: pcg

1	<u>MXKILTA</u> AVV	<u>ALIGILLA</u> IV	<u>LXPDSK</u> TAPA	FSXPDLHGKT	VSNADLQGV
51	TLINFWFPSC	PGCVSXMPKI	IKTANDYKXK	NFQVLAVAQP	IDPIESVRQY
101	VKDYGLPFTV	MYDADKAVGQ	AFGTQVYPTS	VLIQ*GE_LF	KTYVGEPDFG
151	KLYOEIDTRV	AO*			

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m544.pep	MXKILTA	AAVVALIGILL	AIVLXPDSKT	APAFSXPDL	HGKTVSNADL	QGKVTLINFWFPSC
g544	MKKILTA	AAVVALIGILL	ATVLI	PDSKTAPAFSL	PD	LHGKTVSNADLQGKVTLINFWFPSC
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSX	MPKIIKT	ANDYKX	KNFQVL	AVAQPID	PIESVRQYVKDYGLPFTVMYDADKAVGQ
g544	PGCVSE	MPKVT	KTANDY	KNKDFQ	VLAVAQ	PIDPIESVRQYVKDYGLPFTVIYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQV	YPTSVL	IGKXGE	IFKTYV	GE	PDFGKLYQEIDTRVAQX
g544	AFGTQV	YPTSVL	IGKKGE	ILKTYV	GE	PDFGKLYQEIDTALAQX
	130	140	150	160		

1	ATGAAAAAAA	TACTCACCGC	CGCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCGC	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCAACG	CCGACCTGCA	AGGCNAAGT
151	ANCTTGATTA	ANTTTGGT	TCCCTCCTGT	CCGGGTTGT	TGAGCGAAT
201	NCCANAATC	ATTTAAACGG	CAATGACTA	TAAAAACAAA	AACCTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTCCGCA	CACAGGTTTA	TCCGACTTCC	GTCTTTATCG
401	GCAAAAAAAG	CGAAATCCTC	AAAACCTATG	TCGGCGAACC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

```

1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VKNADLQGXV
51  XLIXFWFPSC PGCVMEMXI IKTANDYKNK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGO AFGTOVYPTS VLGKKGEIL KTYVGEFDEG

```

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```

a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T

```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```

a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFLLRKYLV
101 KFIHLHIFTN  IKVFXCVCVK  ELLTILV

```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFLLRKYLFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```

g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcggct  gcggaaaatg  cggcaaaagg  gcaaacgcgc
151 ggtacggata  tgcgtaagg  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaagg  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgtg
251 ttctgtcttt  cggctttacg  cactgtcccg  atgtctgccc  gacagggttc

```

827

```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGCTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CCTTACGGA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSLP GVFLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSLPGVFLAALAAACKPQDNSAAQVASSSASASAENAAKQXTRGTDMRKEDIG
                |||
a548          MFSVPRSLPGVFLAALAAACKPQDNSAAQVASSSASASAENAAKQXTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV
                |||
a548          GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIKQQYRVVSAKVNQXDDSENYL
                |||
a548          FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIKQQYRVVSAKVNQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaaatgc cgctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCGG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTT AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGAGATC GCAAACGGTC
701 ACGTTTTTCG GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGCGCGT AATGATGGCC
851 GTGCCGTGCT GGTCTGCTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FCGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREQYIVH LVREVGAAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVVFV AGLVNHAFCV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVVFVAGL
                                     |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFVAGL
               170      180      190      200      210      220

               40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTGQVQYGGGGNDG
               |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGGNDG
               230      240      250      260      270      280

               100
m550.pep      RAVLVVVEYGDFAAFAX
               |||
a550      RAVLVVVEYGDFAAFAX
               290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactg9 cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggctg9
101 atacgcagaa ttctgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaacgcta tgcggacaaa gcccttgcg9 aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggta gtcgctcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ctggactgca
```

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCCGTCA GTCCGTCGT GCGAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTTELRLI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	QNFDRDIEKNMIEGFNAGFKPYADK				
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	QNFDRDIEKNMIEGFNAGFKPYADK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENV	LDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
a552	ALAEMPEAKKDQAAEAFNRYRENV	LDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKS	MSEIAVSWTALSGKIAQHHLPEFTTELRLI	ICGGKNPDAG			
a552	YGSPVGQSVVAKNPRLIKKS	MSEIAVSWTALSGKIAQHHLPEFTTELRLI	ICGGKNPDAG			
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAAGCCG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
1 LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGVSPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTTELRL IICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

833

```

1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNH
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAFLQNVF FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGTCTTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTGTTG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGTACTTT GTTCCATTTT CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTCGGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
451 ACAAAGAAAA TCAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGFF HTDLRLRQK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCISIKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEEKKE
151 TTKIKILSLR RGXSGLKRSR IQMLILAIISL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGENL				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYGFFHTDLRLRQKYTSLSLKGANL				
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLPC	ILHWDNLNHFVVLESVSSDGA	AVMDPASGR			
m553	ADIMRFGNEMNLTPRALRLELDELSNLQLP	CILHWNLNHFVVLCISIKDS	IVIMDPAVGM			
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELWPNT	RFEAGEEKQEIRILPMLRGISGLGRTL	FQLLALAAAM			
m553	RKIKMDEVSO	KFTGIALELFPNTHFEEKKET	TKIKILSLRGXSGLKRS	LIQMLILAIISL		
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNVF	FKIGRGESLALIGRSGCGKST	LDDILSGNLPPESGKVMIN	GHDIYSLPPP		
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAAATA TATCCGAAAG GCAAAACCGT TCGCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAPAACCGTC CGCGCAGGCT TCTCTAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDN VNLKAGHTE SGGYNLAVSY
251 SGNRHLVI TLGSESAETR ASDNSKLLN ALQAFDTPKI YPKGKTVAQI
301 QISGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSKQILS					
g554	MTAHKILPVLPIIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSRQTL					
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSNG IQSEENLKI PESAWASEGSRMFVRPGDVS					
g554	AKNINTPVEPAALTQLMTAYLVFKNMKSNG IQSEENLKI PESAWASEGSRMFVRPGDVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQOMNKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLAGRLNGSIE NFVQOMNKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNVNLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNVNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNRHLVITLGSESAETR ASDNSKLLN WALQAFDTPKI YPKGKTVAQI					

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	310	320	330	340	350	360
m554.pep	370	380	390			
a554	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccggttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccattcctgct tgcgcgcgtc atcgtcgcgc cgctgcccgg cggttttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKKRPTK QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTCCGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

1	atgaacaaaa	tattccttac	tgcgcgagcc	ttggtgctgg	gcgcgtgcgg
51	tttcacactg	aaaggtgcag	acggcatttc	tccgccgtcg	acctaccgga
101	gctggcacat	cgaaggcgga	caggcatatgc	aatttccctt	ggaaaccgcg
151	ctgtatcagg	cttcgggcag	ggctggacgat	gctgccggcg	cgcagatgac
201	cctgcgtata	gacagcgttt	ccgaaaacaa	ggaacctcat	accgttacc
251	gtgcggcagt	catcaacgaa	tatcttttga	tattgacggt	tgaagcgcag
301	gtattgaaac	gcggcgagcc	ggtcggcaaa	ccgatgaccg	tgctccgtccg
351	ccgcaatttg	gattatgccg	acaacgaatt	tttgggcaaa	caggaagaag
401	aagaaaacct	gtgggcggaa	atgcggcagg	atgttgccga	acagattgtc
451	caccgcctga	ccctttctga	qccgcaatga		

q557.pap..

1 MNKIFLTAA LVLGACGFHL KGADGISPP L TYRSHWIEGG QALQFPLETA
51 LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
101 VLKRGEPV GK PMTVSVRRIL DYADNEILGK QEEETLWAE MRQDVAEQIV
151 RRLTFLKAE*

m557.seq..

1	ATGAACAAAC	TGTTTCTTAC	TGCCGCAGTG	CTGATGCTGG	GCGCGTGCGG
51	TTTCCACCTG	AAAGGTGCAG	ACGGCATTTC	TCCGCCGTG	ACCTACCGGA
101	GCTGGCATCAT	CGAAGGCGGA	CAGGCATTGC	GGTTTCCTTT	GGAAACCCGG
151	CTGTATCAGG	CTTCGGGCGAG	GTGGACGAT	GCTTCCGGCG	CGCAGATGCAC
201	CCTGCGTATA	GACAGCGTTT	CCCAAAACAA	GGAAACCTAC	ACCGTTACCC
251	GTGCGGCAGT	CATCAACGAA	TATCTTTTGA	TATTGACGGT	TGAAGCGCAG
301	GTATTGAAAC	GCGGCAGACC	GGTCGGTAAA	CCGATGACCG	TGTCCGTCGG
351	CCGCGTCCTT	GCTTTATGCC	ACAACGAGAT	CTTGGGCAAA	CAGGAAGAGG
401	AAGCGGCATT	TGTGGCGGAA	ATGCGGCAGG	ATGCCGCCGA	ACAGATTGTC
451	CGCCCGCTGA	CCTTTCTGAA	GGCGGAATGA		

m557.pep..

1 MNKLFLTAAV LMLGACGFHL KGADGISPP L TYRSHWIEGG QALRFPLETA
51 LYQASGRVDD AAGAQM LTRI DSVSONKETY TVTRA AVINE YLLILTVEAQ
101 VLKRGEFVGK PMT VSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

Homology with a predicted ORF from *N. gonorrhoeae*

m557/q557

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGACG	FHLKGADG	ISPP	LTYSWHIEGG	QALRFP
	ETALYQAS	GRVDD				
	:	:				
g557	MNKIFLTA	AALVLGACG	FHLKGADG	ISPP	LTYSWHIEGG	QALQFP
	ETALYQAS	GRVDD				
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM	TLRIDSV	SQNKETY	TVTV	TRAAVIN	EYLLIL
	TVEAQV	LKRGE	PGVKP	MTVS	VRRVL	
						:
g557	AAGAQM	TLRIDSV	SQNKETY	TVTV	TRAAVIN	EYLLIL
	TVEAQV	LKRGE	PGVKP	MTVS	VRRIL	
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNE	ILGKQ	EEEEAL	WAEMRQ	DAEQIV	RRLTFL
	KAEX					
			:			
g557	DYADNE	ILGKQ	EEEEET	LWAEMR	QDVAEQ	IVRRLT
	FLKAEX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1641>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558 / q558

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

```
a558.seq
  1  ATGAATGCTT  GTTTTTCGT  CATCCCA  CAGGCGGAA  TTCGAGATT
51  CGGGAATTGT  TTCAAACGT  CGGGTCGGAT  TCTTGCCGT  GCGGGAATGA
101 TGCCCTTATA  TATAGTGGAT  TAAATTTAA  TCAGGACAAG  CGCAGCAAGC
151 CGCAGACAGT  ACAAATAGTA  CGGCAAGCG  AGGCAACGCC  GTACTGGTTT
201 AAATTTAATC  CACTATACTT  TCTCCGAGCT  TTATATGTTT  CAACAGAGGA
251 CGGCACATCA  AGCACCGCAC  TGCGTGTTC  CCGAACGAGA  CTGCCCTCCG
301 ATTAGATTCC  ATCGCTATAA  ACAGACGGGT  TTCAACCGAA  AAGGAATGGG
351 AATGAAGTCC  GTTTCGACA  CCTTCTGCC  GATGCCGTCT  GAAACCAAT
401 CTCCACTTTC  AGACGGCATT  GTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

```
a558.pep
1  MNACFFVIPT QAGIRRFQIV FKRSGRILAG AGMPLYIVD *I*IRTRRS
51  RRQYK*YGKA QRRTGLNLI HYTFSELYMF QQRTAQHQP CVLPERDCFP
101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPSLDGI V*
```

m558/a558 70.2% identity in 141 aa overlap

```

      10       20       30
m558.pep  MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLY-----
          |||||
a558      MNACFFVIPTQAGIRRFGIVFKRSGRILAGACMPLYIVDXIXIRTRRRSRROYKXYGKA
          10       20       30       40       50       60

      40       50       60       70       80
m558.pep  -----TFSELYMFQOGTAHQAPHCVLPERDYPPIRFYRHKTGFNRKGMGIKS
          |||||
a558      RQRRTGLNLIHYTFSELYMFQORTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS
          70       80       90       100      110      120

      90       100
m558.pep  ISDIXRAMPSENQSPLSDGIVX
          :|| |
a558      VSDTSRAMPSENQSPLSDGIVX
          130      140

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1649>:

g560.seq
1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```
a560.seq
1  ATGCTCATCA  TCCGCAACCT  GATTTACTGG  CTGATACTCT  GTTCCACCCT
51  GATTTTCCTC  TTCCCTTATA  TGCTGCTCGC  CTCGCCTTTC  CGAGACGGGG
101 CGCACAAAGAT  GCGCGGGGTC  TGGGTCAAAA  TCCTCAACCT  CTCGCTCAAA
151 CACATCGTCG  GGCTCAAATA  CCGCATCATC  GCGCGGGA   ACATCCCGGA
201 CCGCCCCGCC  GTCATCTGCG  CCAAACACCA  AAGCGGCTGG  GAAACGCTCG
251 CCCTTCAGGA  CATTTTCCG  CCGCAGGTTT  ACGTTGCCAA  ACGCGAGTTG
301 TTCAAAATCC  CCTTTTCGG  CTGGGGCTTG  AAACCTGGTC  AAACCATAGG
351 CATAGACCGC  AACAAACGCC  GCGAAGCCAA  CGAGCAGCTC  ATAAACAGG
401 GGTGCGCGCG  CAAAAACGAA  GGCTATTGGA  TTACCATTTT  CCCCAGAGGC
451 ACACGCCITG  CGCCCGGAAA  ACGCGGCAAA  TACAACTCG  GCGCGCGCGG
501 CATGGCGAAA  ATGTTTGAGA  TGGACATCGT  CCCCCTCGCC  CTCACAGCG
551 GCGAATTTTG  GCGAAAAAAC  TCCTTTCTGA  AATATCGGG  GGAAATCACC
601 GTCGTATCT  GTCCGACCAT  CCGCACGCA  AGCGGCAGCG  AAGCCGAATT
651 GATGGGAAA  TGCGAACACC  TCATCGAAAC  GCAGCAGCCG  CTCATTTCCG
701 GCGCAGGCC  GTTGCCGCC  AAAATGCCGT  CTGAAACCGC  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```
a560.pep
1  MLIIRNLIYW  LILCSTLIFL  FPFMLLASPF  RDGAHKMARV  WVKILNLSLK
51  HIVGLKYRII  GAENIPDRPA  VICAKHQSGW  ETLALQDIFP  PQVYVAKREL
101 FKIPFFGWGL  KLVKTIGIDR  NNRREANEQL  IKQGLARKNE  GYWITIFPEG
151 TRLAPGKRGK  YKLGARMAMK  MFEMDIVPVA  LNSGEFWPKN  SFLKYPGEIT
201 VVICPTIPHA  SGSEAELEMG  CEHLIETQQP  LISGAGPFAA  KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

845

501 QESLSNIRKH ARATHVKFTL SEHGGRTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY					
g561	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
g561						
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
g561	:	:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWWIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
g561						
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONQLTLLYQTTDRDLHQSYPQAAEHFLNRLPAVGADSGRVCLDG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTGCGC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	CCCGGAAACA	TCGAACTGTT	TTTGACGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATG
501	GGCAATTATG	TTGATGACGC	TGGTGTGCTC	TGTAATGATG	CTGTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTGCGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGACCGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCATTT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGACAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAACAAA	CGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
	WENGSLPPEAQLOMIFILOESLSNIRKHARATHV KFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQT TVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQT TVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. glaucochromae* <SEQ ID 1659>:

g562.seq..

1	atggcaagcc	cgctcagatct	gcctttcaat	tcgggcaaga	ccaaaccgac
51	ggcttttgcc	gcgccggttt	tggtcggaa	catgttttcc	acgcccgctgc
101	gggcgcgcg	caggtctttg	tggcgcacgt	cggtaacggt	ttggtcggtg
151	gtcagtcgct	ggatggtggt	cattgcgcct	ttgacgatgc	cgacgctttc
201	gctcaacact	ttggcaaccg	gcgagaggca	gttgggtggtg	caggaagcgt
251	tggaacgac	ggtcatgtcg	gcggtcagga	cgctgtcgtt	cacgccgtac
301	acgacggtt	catcgacatc	gtcgccgccc	ggtgcgga	tgaggacttt
351	tttcgcgccg	ctttcgaggt	ggattttggc	ttttctttg	ctggtgaacg
401	cgccggtgca	ttccatgacc	aaatcgacac	cgagttcttt	ccacggcagt
451	tcggcaggt	tgccgggtcga	gaagaagggg	attttgtcgc	cgttgacgat
501	gaggttgccg	ccgtcgtggg	atacgtcggc	ttcaaagcgt	ccgtgtacgg
551	tgtcgaattt	ggtcagatgg	gcgttggttt	caaggctgcc	gctggcggtg
601	acggcgacga	tttgaggtg	gtcttga		

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

1	MASPSL	LPFN	SGTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMV	VIAP	LTMP	TL	SLNT	LATGERQLVV
101	TTVAST	SSPP	GAEMRTFFAP	LSRWILAFSL	LVNAPVHSM	T
151	SAGLRV	EKKG	ILSPL	TMRLP	PSWDT	SASKR
201	TATIWS	WS*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

1	ATGGCAAGCC	CGTCGAGCCT	GCCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCGTTT	TGCTCGGAAT	CATGTTTCC	ACGCCCGTGC
101	GGGCGCGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCAGAGAGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAACGAC	GGTCATGTCG	GCGGTCAGGA	CGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTTCGAGGT	GGATTTTGGC	TTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCGA	GAAGAAGGGG	ATTTTGTGCG	CGTTGACCAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTCAGATGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	GTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

1	MASPSL	LPFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMV	VIAP	LTMP	TL	SLNT	LATGERQLVV

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	70	80	90	100	110	120
m562.pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
m562.pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
m562.pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200	209			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTCTG TTAATCAATA
351 TGCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TTCAAGGCAA TCCTTGCTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAAC TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTACAC GTATTCTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 AACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTACAG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTCGG
1351 ATTAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAAACAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCCGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAC TGCGCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
5301 TCAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAAGTGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTT
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATTC TCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCAgCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAACCTA ACCGCCAGTC AagaAACCCG TCACGTTCTT
5851 GCCCAGCGCG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag
6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggta cGgctGCCGG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGT TGTTTTcaaa
6101 cggtTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

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1 MNKTLYRVIF NRKRGAUVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51 SKAFCFSALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNIP
101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNNGGFIN
201 ASRATLTTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQGQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLSN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTQ IQAQGMNNIG
501 TGRIYGDNIA IAATRLDNQD ENGTGAALAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGGA LDNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVFNYN ESDHLRTPDG
651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNWYRARRK GHDETGHREQ
751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS
801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGSYDM
851 LGSLKLDPNP LHKRLGDGYY EORLINEQIA ELTGHRRLDG YQNDDEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQSAVTAT QDINNIGGIL SAEQTLNLA GNNINNQSTA
1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINI AGQISNQSDQ
1101 GQTRLQAGRD INLDTVQTGK YQEIHFDAVN HTIRGSTNEV GSSIQTGKDV
1151 TLLSGNNLNA KAEVGSAGK TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
1201 SGGGNKLVI DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
1251 TRIQAGNHVR IGTQTQSQS EYHQTQKSG LMSAGIGFTI GSKTNTQENQ
1301 SQSNEHTGST VGSLLGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMDIG
1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVQSKN
1401 DRVNAMAAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQONRQTT
1451 QVQANQAQAS QIQAGGKTL YCRRCEQSN INITGSGVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSONKSA GWNAGAAVSF GQGGWSLQVA AGGNVKGKYG
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIIK GAQVRGKGVQ VNAKNLSIQS
1601 VQDRETYQSK QNAGAQVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTSTGTLA GSDIQNYSQY
1701 EKSFLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKNGA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTTDTAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KAVQQTNTEI NOHLDKLDKAD
1851 KEAAETAAAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQANAGKL TASQETAHVL
1951 AHAVLGAAVA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KGDGGSLNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVLG CFQTASDFAS SFSYPINM*

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3001  GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
3051  GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT
3101  TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTTCATT TGCCTATGAA
3151  TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201  GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251  CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
3301  CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG
3351  TGACTATATG CTGGACAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC
3401  GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA
3451  GAGCTGACAG GGCATCGTCG TTAGACGGT TATCAAAACG ACGAAGAACA
3501  ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC
3551  TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
3601  GATATTGTTT GGTGTTGACA AAAAGAAAGT AAGCTTCCTG ATGGCGGCAC
3651  ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
3701  TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT
3751  TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT
3801  TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA
3851  AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
3901  TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA
3951  AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
4001  ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA
4051  GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA
4101  ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
4151  ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201  CATGTTATTG GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251  AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
4301  AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC
4351  AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401  CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451  AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
4501  GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTC
4551  CGATAATGGC ACCCAGATTC AAGCAGGCAA TCATGTTTCG ATTGGTACAA
4601  CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
4651  TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA
4701  AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751  TGAAAGGCGA TACCACCAT GTTGCAAGCA AACACTACGA ACAAATCGGC
4801  AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851  AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT
4901  ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCGT TACCGATTTG
4951  GCACAACAAG CGATTGCCGT AGCACAAGC AGCAAACAAG TCGGACAAAG
5001  CAAAACGACG CGGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051  CCTATCAAAC AGGTAAGAGT GCACAAACT TAGCCAATGG TACAACCAAT
5101  GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151  AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG
5201  GTGGTAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
5251  AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
5301  CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
5351  GCCAAACAA ATCGGCAGGC TGAACGCAG GTGCTGCCGT ATCATTGCGA
5401  CAAGGAGGCT GGTCAATTAG CGTTACCGCA GGCGGCAATG TCGGCAAAGG
5451  CTACGGCAAT GCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA
5501  AAGGCAGCCA AACCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551  GCGCAAGTAC GCGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601  TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACA CAAACGCCA
5651  GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
5701  CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751  TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTGCGAAAC CATACAGACC
5801  TCAAAGGCGG CATCATACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA
5851  AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCACAG
5901  CCAATACAAA GCGGAAAGTT TTGGATTGGG CGCAAGTGCG TCCATAACCG
5951  GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG
6001  ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051  CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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855

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1551 LMSAGIGFTI GSKTNTQENQ SOSNEHTGST VGS LKGD TTI VAGKH YEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNK LNSNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAI A VAQS SKQVQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSI SITY GEQQNROTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSN I
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNK SAG WNAGAAVSFG
1801 QGGWSLGVTA GGNVGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYOSQO QN ASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGK
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDK LKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGKV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFKDLA
2201 QONANGK LTA SQETAHVLAH AVLGA AVAAV GDNNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGA AVGN SATDAAQGS L
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VHKDPGSTLE PNISTIASTF
2351 QLNLFNSEF GEGGVGN AF RHVLWOATIT REFGKDI AVK VGNSHESGEK
2401 INYSIRNLS LDKADEMIDQ LNNEIGKEIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563 . pep  MNKTL YRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563 . pep  MNKTL YRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90     100     110
g563 . pep  FSALGFSLCLALGTVNIAFADGII TDKAAPKTQQATILQTGN GIPQVNIQTPTSAGVSVN
              || |||||
m563 . pep  FSL LGFSLCLAVGTANIAFADGIIADKAAPKTQQATILQTGN GIPQVNIQTPTSAGVSVN
              70      80      90     100     110     120

              120     130     140     150     160     170
g563 . pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563 . pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563 . pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL
              |||||
m563 . pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563 . pep  DARDTDFTRIL-----
              |||||
m563 . pep  DARDTDFTRILSYHSKIDAPVWGQDVRV VAGQNDVVATGNAHSPILNNAANTSNNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563 . pep  -----LYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              : |||||
m563 . pep  GTHIPLFAIDTGKLGGM YANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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857

g563.pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSSENGKLHNYWRARRK
m563.pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
g563.pep	750 760 770 780 790 800
	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563.pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSQGTLPQSN-----
	1030 1040 1050 1060 1070
g563.pep	810 820 830 840 850 860
	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563.pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLDPNN
	1080 1090 1100 1110 1120 1130
g563.pep	870 880 890 900 910 920
	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEQFKALMDNGATAARSMNLSVGIAL
m563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
g563.pep	930 940 950 960 970 980
	SAEQAAQLTSDIVVLVQKEVKLPDGGTQTVLMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563.pep	SAEQVAQLTSDIVVLVQKEVKLPDGGTQTVLVPQVYVRVKNGGIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
g563.pep	990 1000 1010 1020 1030 1040
	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQKSAVTATQDINNIGGILSAEQTLNNA
m563.pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQKSAVTATQDINNIGMLSAEQTLNNA
	1260 1270 1280 1290 1300 1310
g563.pep	1050 1060 1070 1080 1090 1100
	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAQAGKDINIAGQISNQSDQ
m563.pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAQAGKDINIAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
g563.pep	1110 1120 1130 1140 1150 1160
	GQTRLQAGRDINLDTVQTKYQEIHFADNHTIRGSTNEVGSSIQTGKDVTLLSGNNLNA
m563.pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQTGKDVTLLSGNNLNA
	1380 1390 1400 1410 1420 1430
g563.pep	1170 1180 1190 1200 1210 1220
	KAAEVGSAGKTLAVYAKNDITISSGIHAGQVDDASKHTGRSGGKNLVIITDKAQSHHETA
m563.pep	KAAEVSSANGTLAVSAKNDINISAGINTTHVDDASKHTGRSGGKNLVIITDKAQSHHETA
	1440 1450 1460 1470 1480 1490
g563.pep	1230 1240 1250 1260 1270 1280
	QSSTFEGKQVVLQAGNDANILGSNVISDNGTRIQAAGNHVRIGTTQTQSQSEYHQTQKSG
m563.pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTQIQAAGNHVRIGTTQTQSQSEYHQTQKSG
	1500 1510 1520 1530 1540 1550
g563.pep	1290 1300 1310 1320 1330 1340
	LMSAGIGFTIGSKTNTQENQSQSNHEHTGTVGSLKGDTTIVASKHYEQTGSNVSSPEGNN

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m564.seq
1 ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51 GATACCGCGT GCTGAAAATG CCAACCGCGA GGGCAAAAAA ACAGCCGCACA
101 CCAAGAGCTG AGGTATTTTG CCAATGATA TTGGCGGGTT TCGGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTT
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACCAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GCGATACCCG AAGTCAATAT TCAACACCCCT ACTTCGCGAG GGGTTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGTTGG CAAGGGGCGA AGCAGCTGTG GTTGTAACC AAATCAACAG
501 CAGCATTCTT TCACAACCTA ATGGCTATAT TGAAGTGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGCGAGGTA TTGCAGTCAA TTGCTGGTGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTTGAGTGCA CGGTATACCG ATTACACACG TATTCCTCAGT
751 TATCATTCCA AAATTGATGC ACCTGATGG GTACCAAGATG TTCGTGTCTGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATCAGGCG AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA TGACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAATCTGGTA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATCGCGT
1101 TTCACTTCAT GCCCGCAATG TTCATAATG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTGAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACCGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA TTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAG AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACCAATCCG TTTCACTTAC AGCACTGCA AAAAATCAG CCGTAGGACG
1551 CATTCAAACA ATCCAGGCAT TTGACAATGC AGGATCAATT AATGCGGGT
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGGTA AACTACGAGT ATCAGCGCAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACAGC ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAAC TCAACCGGCA AGATTGATAA CCGTGAACGT
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTGGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATCGCAGTA ACATTCTTGC CGATAGTGGA
1951 ACCGTTACCA CCAAGAATAA TCTTCGAACT ACAGGAAAGG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG TACCCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACCGC AAATCCTTAT CTGCAAAATC AGCACAATTA GCTGTTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT
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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAACCG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CGGCGGCTGG GACGCGCAGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCTG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTCTTACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCGAGCCG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GCGCGCGCGG GGCCTTCCC
7001 TTGCCGCACC GTATTGGAC AAAGCGCGG AAAACCTCGG TCCGCGCGG
7051 AAAGCGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTG AACATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCGAGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGCGAGCG ATCCCTTATT GCGGGGTGCG GGGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAQG NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPVPIQ IPSTATSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHDLAVENTQ TAKNSGHLLT QTKIDNSREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLNQSG
701 HITATEQLTI NSRNVNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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865

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1350      1360      1370      1380      1390      1400
m564 .pep  T L S D G S T Q T V L V P K V Y A L A R K G D L N T S G G L I S A E Q V L L K L Q N G N L T N S G T I A G R Q A V L I Q
           : | : : | | :           | : | : | : : : | : | : : | | | : : : : | :
fhab_borpe --ENGASVTVRTT-----GNLVNKGYISAGKQGVLEV-GGALTNEFLVSGDGTQRIE
           1260           1270           1280           1290           1300

1410      1420      1430      1440      1450
m564 .pep  A R N I N S N G N I Q -----A D Q I G L K A E K S I N I D G G Q V Q A G R L L T A Q ----A Q N I N L N G T T
           | : | : : | : | : | : : | | : | : | : | : | : | : | : | : | : | : | : | :
fhab_borpe A Q R I E N R G T F Q S Q A P A G T A G A L V V K A A E A I V H D G V M A T K G E M Q I A G K G G S P T V T A G A K A
           1310      1320      1330      1340      1350      1360

1460      1470      1480      1490      1500
m564 .pep  Q T S G N E R N G N T A I - D R M A G I N V V - G S H T E Q V D N R T S D - G I L S L H A S N D I N L N A A T V S N Q V
           | | : | : : : | : | : : : : | : | : | : | : | : : : : | : : : | : |
fhab_borpe T T S A N K L S V D V A S W D N A G S L D I K K G G A Q V T V A G R Y A E H G E V S I Q G D Y T V S A D A I A L A A Q V
           1370      1380      1390      1400      1410      1420

1510      1520      1530      1540      1550
m564 .pep  --K D G T T Q I T A G N N L N L G T - I R T E ---H R E A Y G T L D D E N H R H V R Q S T -----E V G S
           : | : : : : : : : : : | : | : : | : | : : : : | : : : : | : : : : | : :
fhab_borpe T Q R G G A A N L T S R H D T R F S N K I R L M G P L Q V N A G G P V S N T G N L K V R E G V T V T A A S F D N E T G A
           1430      1440      1450      1460      1470      1480

1560      1570      1580      1590      1600
m564 .pep  S I R T Q N G A L L R A G N D L K I R Q G E L E A E E G K T V L A A G R D V --T I S E G R Q I T E L D T S ---V S G
           : : : : : | : | : : : : | : : : : | : : : : | : : : : | : : : : | : :
fhab_borpe E V M A K S A T L T T S G A A R N --A G K M Q V K E A A T I V A A S V S N P G T F T A G K D I T V T S R G G F D N E G
           1490      1500      1510      1520      1530

1610      1620      1630      1640      1650      1660
m564 .pep  K ---S K G I L S S T K T H D R Y R F ---S H D E A V - G S N I G G G K M I V A A G Q D I N V R G S N L I S D K G I
           | : | : : | : : : | : | : | : | : : : : : | : : : : | : : : : | : :
fhab_borpe K M E S N K D I V I K T E Q F S N G R V L D A K H D L T V T A S G Q A D N R G S L K A G H D F T V Q A Q R I --D N S G
           1540      1550      1560      1570      1580      1590

1670      1680      1690      1700      1710
m564 .pep  V L K A G H D I D I S T A H N R Y T G -----N E Y H E S K K S G V M G T G G L G F T I G N R K T T D D T D R T N I V
           : : | | | | : : : | | | | : : | : : : : | : : : : | : : : : | : : : : | : :
fhab_borpe T M A A G H D A T L K A P H L R N T G Q V V A G H D I H I I N S A K L E N T G R V --D A R N D I A L D V A D F T N --
           1600      1610      1620      1630      1640      1650

1720      1730      1740      1750      1760      1770
m564 .pep  H T G S I I G S L N G D T V T V A G N R Y R Q T ----G S T V S S P E G R N T V T A K S I D V E F A N N R Y A T D Y A
           | | | : : : | : | : | : | : | : : : | : | : | | | : | : : : : | : :
fhab_borpe -T G S L Y A E H D A -T L T L A O G T Q R D L V V D Q D H I L P V A E G T L R V K A K S L T T E I E T G N P G S L I A
           1660      1670      1680      1690      1700      1710

1780      1790      1800      1810      1820      1830
m564 .pep  H T Q E Q K G L T V A L N V P V V Q A A Q N F I Q A A Q N V G K S K N K R V N A M A A A N A A -W Q S Y Q A T Q Q M Q Q
           : | | : : : | : | : | : : : | : : : | : | : | | : | : : : | : : : | : :
fhab_borpe E V Q E -----N I D N K Q A ----I V V G K D L T L S -S A H G N V A N E A N A L L W A A G E L T V K A Q N
           1720      1730      1740      1750

1840      1850      1860      1870      1880      1890
m564 .pep  F A P S S A G Q G Q N N N Q S P S I S V S I T Y G E Q K S R N E Q K R H Y T E A A A S Q I I G K G Q T T L A A T G S G
           : : : : | : : : : : : : : : : : : : : : | : : : : | : : : : | : :
fhab_borpe I T N K R A A L I E A G G N A R L T A A V A L L N K L G R I R A G E D M H L D ---A P R I ----E N T A K L S G E V
           1760      1770      1780      1790      1800      1810

1900      1910      1920      1930      1940      1950
m564 .pep  E Q S N I N I T G S D V I G H A G T A L I A D ---I R L Q S A K Q D G S E Q S K N K S G W N A G V A V K I G N G I R F
           : : : : : | : : : : : | : : : : | : : : : | : : : : | : : : : | : :
fhab_borpe Q R K G V Q D V G G E H G R W S G I G Y V N Y W L R A G N G K K A G T ----I A A P W Y G G D L T A E Q S L I E V
           1820      1830      1840      1850      1860

```

867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRATAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565          MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRATAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTCEFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

```

869

```

g566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCGCGCG GGACGCTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AACGCGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHAX*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq.
1  atcgacgac gggcagcggc atcgacaagg cgggtttgca gtcggcggtt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtagcgag
101 caaagagggc ggatacggcg tggtgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgcttcgct gacgctgttg acgcttaacg gcttggtggc ggcgggcggc
301 gtgattgtgc cgatgttggt cgaatattac gcgctggaag ggatttcgga
351 tttgattgca accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcggtcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcgaata tccgccttgc ggaagcgccg agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa ggcgtatctt
601 gccttggcgg acgaactggc ggcgagggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSR RYAAKRADTA CWVRTRALAG
51  AEIELVQEI REVLKLNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDTIGIVR TMYDSRSRLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

871

```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCAGG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTGCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGRVRLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSHEFDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKG KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep    MSANILAIANQKGGVGKTTT TVNLAASLASRGRVRLVVDLDPQGNATTGSGIDKASLQSG
              |||
a567         MSANILAIANQKGGVGKTTT TVNLAASLASRGRVRLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep    VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||
a567         VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep    DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              |||
a567         DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep    GIVRTMYDSRSRLVAEVSEQLRSHEFDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||
a567         GIVRTMYDSRSRLVAEVSEQLRSHEFDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep    KAYLALADELAARVSGKX
              |||
a567         KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgtctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
 51 gataccttgc agaattctgcc gattaaagcg ttccgcggtg cccaatatct
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaaagcc
151 tgtaaaaaca gccccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatatct tccaacgcgt ccaagccgct tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggcgtg tgcggtccat
351 aattacggcg atgtgcctcg ggatggcggg gtgttccaaa atggtctgcg

```

873

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGTAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GGCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGCGG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGCTCTG
451 AACGCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCG CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCTTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCTIF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFEDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
	250					
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgcctt gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCCTTAT GGTTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

a569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGIC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGICKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGICKIKTNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHFDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
a569	ALVSLRPHFDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m569.pep	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLSWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLSWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1 atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacaggc gcgcacgcg acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaaa ggcagctcgc cggcgggcaa ctttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

```


877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
  51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
 101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

                10      20      30      40      50      60
m570.pep      MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
                |||||
a570           MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
                10      20      30      40      50      60

                70      80      90     100     110     120
m570.pep      ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
                |||||
a570           ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
                70      80      90     100     110     120

                130     140     150     160
m570.pep      SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
                |||||
a570           SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
                130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tcggcgccgg
  51  tataggttct gccgtcccac acgctgcctg cgtcggaaca caggctcagg
 101  cggacgggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
 151  ggagacgttg gcttttttgt tgcgcgcgta gctgattttt tcgcccattt
 201  cgtcatacac ttccgggccg agcgtgccgc ttccgtagcc gcgcaccgaa
 251  cccaggccgc cgcgcgtaga gttttcaaa aaggggattt ctttggttct
 301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
 351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
  51  GDVGFFVAAV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
 101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGG CCGGTCGCGG
  51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACAGCT GCCTGCGTCG
 101  GCAAAACAGG TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
 151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
 201  TTTTTCGCCC GTATTCGTCA TAGACTTTTC GACCGAGCGT GCCGCTTTCG
 251  TATCCGCGCA CCGAACCCAG GCCGCGCGCG TAGAAGTTT CAAAGAAGGG
 301  GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
 351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAAGT TTGGTTGTGG
 401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCCGCGTT
 451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
  51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
 101  DFFGSAVAAR NADFAAEHQE EGFAQGEE?G LVVGGGVVLQ FAARQGDGFGV
 151  HARQVAARRP *

```

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```

1  atgtgcgcca tcgtcggggc ggcggggctg ccttcgcgc tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctgggtggtt
101 cccgcgcgtt gtttatggaa accgccgcg caaacggcgc ggcagtggtg
151 cccgtcgaca gcgaacacaa cgccatttgc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgcccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 ccgagcgagg cgggtcaaca ccccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccat tgtttgggct
551 tgcccgagcg catcgattcg ggtgtcggca aactcgattt cggcgcatcg
601 tcgcgcgtga ccttcacaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaaccgcc gtccgcgcct ttttggacgg acagattaag
751 tttaccgaca ttgccaaaac cgtcgccac tgcttgcac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccgacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

```

g572.pep.
1  MCAIVGAAGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYDTR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDGAL
201 SALTFOKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

```

m572.seq.
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TCTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGTG
151 CCGTCGACA GCGAACACAA CGCCGTTTC CAAGTTTGC CGCGCGATTA
201 CGCCGCGCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTGA CCGCATTACG
301 CCGCCCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC CATCGCTTAT TGTGTGGTT
551 TGCCCGAGCG CATCGATTTC GGTGTCGGCG ACCTGSATTT CGACGCATTG
601 TCCGCGCTGA CTTTCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAG
651 GCTCGCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCCGCGCCT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCAC TGTCTTGAC AAGACTTTTC
801 AGACGCATA GCGATATAG GGGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGCACAAAG GCGAGCATTT ATCGGCACAC TGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

```

m572.pep.
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFOKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVL PVDSEHNAVF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLUVSGALFMETARANGAAVL PVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       QVLPRDYDRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGGQIKFTLIAKTVAHCLAQDFSDGIGDIGSLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGGQIKFTDIAKTVAHCLSQDFSDGIGDIGSLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctggt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atg.ccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaaccgg tcggaccggg taccagcacc atcccgtaa gacgggtgaat
301 cgcttccaac acaaatTTTT tctggaacgg ctcaaaacgg agctgggtcga
351 tgttcaaga cgcgcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgTTTTTCGG
501 aaatgtccaa acgcgacatt accttaatcc gggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgagg agctgcccgt ccacacggaa
601 acggatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcatccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtcgatatac aggggtgtgc tttcctcttc
751 ctcttgcccc tccccaagct cctgaagcag cgatgtcgaa cgcgaaacca
801 cccaatcgag caaacccgcc aactggctat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctgggt
901 cggatcgga accgcacaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctccg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacacctt
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN IGSFQITNLT DHNDVRLVLTQ ERLQSSGKSQ TLLIIDVNLII
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPFPGNVQ TRHYLNPGSK LPPYRNRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTAAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACCGTGAAT
301 CGCTACCAAC aCaw.TTTTT TCTGAAACGG CTCA.ACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

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a573.seq

```

1  ATGCCCTGTT TGTGCCCTCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAACAGG TATAGAGCGA CACCGTCTTA
251 CCGGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAGG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNECGR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQTLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFLLKRLKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNXPXSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCTG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGAAAA
1051 GCCGATGCCG ACATGATGCG TTCGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1  MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

m574.pep	10	20	30	40	50	60
	MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA KSIPSGFYKS					
g574	10	20	30	40	50	60
	MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA KSIPSGFYKS					
m574.pep	70	80	90	100	110	120
	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
g574	70	80	90	100	110	120
	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
m574.pep	130	140	150	160	170	180
	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGKMAREA RQHLLNIYQQ DRDWEKAVET					
g574	130	140	150	160	170	180
	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGEMAREA RQHLLNIYQQ DRDWEKAVET					
m574.pep	190	200	210	220	230	240
	ARLLSHDDQT YQFEIAQFYCE LAQAALFKS NFDVARFNVG KALEANKKCT RANMILGDIE					
g574	190	200	210	220	230	240
	AQLLSHDDQT YQFEIAQFYCE LAQAALFKS NFDVARFNVG KALEANKKCT RANMILGDIE					
m574.pep	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
g574	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
m574.pep	310	320	330	340	350	360
	INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK ADADMMRSVI					
g574	310	320	330	340	350	360
	INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK ADADMMRSVI					
m574.pep	370	380	390	400		
	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKIEVX					
g574	370	380	390	400		
	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKIEVX					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDLDPWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFPTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFPTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1 ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 ccgtaaaca gtccgcttcc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggctgtt tccgaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtct cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttcagc gggtacaggt cgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggcgg gtttttcggc
351 ttttgcctcg ggcgcggcaa cttttgtctc aggtttttca accggttttt
401 cgacaggttt ctctatcggg ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggccttgggt ttgcgcgttt gcggtttggg
501 ttgttcgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1 ..MPCLRRQAAR CTNRRTDRQT VRFRLLRQK PVRQVRQVR RQLHLWLPQQ
51 VRKRCYRFRR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGS RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq .
1 ATGTTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TGTGTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTTCACAGG
201 GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGTGTCT GTGGATTGGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCTCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGGG TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGACCGTC AAACAGTCCG TTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTAT GGCAGAAGCG GCGGCTTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 TCGCAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTGTTGGGT
1001 GTTCCGCTT GATCCTGTT AGATTCGAA TGTGA

```

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m575/a575 98.8% identity in 344 aa overlap

```

      10      20      30      40      50      60
m575.pep  MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV
          |||
a575      MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m575.pep  SMTISTGLYGLKVSGSYTLSDVSMFQASARFWVSSSCVSAAPDKMPFCAAARLSKSKSM
          |||
a575      SMTISTGLYGLKVSGSYTLSDVSMFQASARFWVSSSCVSAAPDKMPFCAAARLSKSKSM
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m575.pep  RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR
          |||
a575      RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m575.pep  SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPNRPNSPLSVSSSAETC
          |||
a575      SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPN----SPLSVSSSAETC
          |||
      190     200     210     220     230

      250     260     270     280     290     300
m575.pep  STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA
          |||
a575      STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA
          |||
      240     250     260     270     280     290

      310     320     330     340
m575.pep  SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX
          |||
a575      SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX
          |||
      300     310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggctgtg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcctgcagg agcagcaggg taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgcccgcc
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccctccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtcggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITY
101 QGEGKQPTKD DIIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

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601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
  51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITYKQE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
a576                                CGKKEAAPAS ASEPAAASSA QGDTSSIGSTMQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
a576 FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m576.pep KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
a576 KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
a576 VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
                                210     220     230     240     250     260

                                220
m576.pep KQPAQVDIKKVN
a576 KQPAQVDIKKVN
                                270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
  51 ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 ACAAATGAAG GAACAGGCGC CGGAAATCGA TTTGAAAGTC TTTACCGATG
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
 301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
 401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
 451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTAGGCCAA
 601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

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```

1  ATGAACACCA TTTTAAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCGCGCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGCGC CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KGVKTTASG
151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSEKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASSAAGDT	SSIGSTM
m576-1	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASSAAGDT	SSIGSTM
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQMK	EQGAEIDL	KVFTAMQ	AVYDGKE	IKMTEEQA	QEVMMKF
m576-1	DIGRSLQMK	EQGAEIDL	KVFTAMQ	AVYDGKE	IKMTEEQA	QEVMMKF
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKE	KGEAFLE	NAAKDGV	KTTASGL	QYKITKQ	GEGKOPT
m576-1	KADAKANKE	KGEAFLE	NAAKDGV	KTTASGL	QYKITKQ	GEGKOPT
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSK	ANGGPVT	FPLSQV	ILGWTEG	VQLLKEG	GEATFYI
m576-1	GTVFDSSK	ANGGPVT	FPLSQV	ILGWTEG	VQLLKEG	GEATFYI
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVK	LVKIGAP	ENAPAK	QPAQVDI	KKVNX	
m576-1	ATLVFDVK	LVKIGAP	ENAPAK	QPAQVDI	KKVNX	
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

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```

|||||
g577      YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100      110      120

          130      140      150      160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||:|||||
g577      LSLRGENSRRLRAEVKKARLSGQKLTAPPIQNAAESAKQPX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAATTT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAGTAGC   GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAAATTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTTCGGCG  CGTTTGTCTG  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TGCGGTTTGT  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSEKLAQSW  FRVRSCTPGGV
51  FIYGANMKLI  YTVIKIIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGRL  LSLRGENGRL  RAEVKKNARL  TGKELTAPPA
151 QNAPESAKQP  *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
          |||||
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCTPGGVFIYGANMKLI
          10      20      30      40      50      60

          70      80      90      100     110     120
m577.pep  YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL
          |||||
a577      YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100     110     120

          130     140     150     160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcg
151 gcggatttcg  ctctcgtgt  atttcattgt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcgggt  cgccgaaata  aatatcgccg
251 gtaagttcgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcaggctt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFVVFHG  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDFRL

```

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```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCGGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCGGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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```

1  ATGGACTTCA AACAAATTTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGCGGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGAATATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC TAAAAGACC AGCTGTCCAA
351 TTTTGGCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCAGC CTGCCGCTTT
551 GCGCGCCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAAGTGGT GAAAACCTCC GCAAATCAA
801 TATCAACATC CCGTCCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVLPNSV V MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE ROPAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAAATTTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGCGGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTCTTGGTC GGAATATGGG CGGCGAAACG CATTGTCGCT
151 GTSATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGTT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGGCGCC GCGCGACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCGCGCCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAAGTGGT GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVLPNSV V MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1						
	10	20	30	40	50	60
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVLPNSVVMGNSIVNRST					

901

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaatattg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc cggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCCC ACGCCACTTC GGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101  *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS
          |||
g580       MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90     100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX
          |||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX
          70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTGCGTT TCGCCACCCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCGW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGGTGA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTACCAC GTTTCGGGC
301 CGCATCGCA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGF	TRVNMGGN	TDVTVQADRG	LSHFISLSK	LETEVRECFV	
a581	MHFAQLVGQTGIEQNTFCRRGF	TRIDMGGN	TDVTVQADRG	LSHFISLSK	LETEVRECFV	
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQ	VHGFLLTFAG	RINPAHCQS	QQTAX	
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQ	VHGFLLTFAG	RINPAHCQS	QQTAX	
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgcttttgc ggacaaatgt acgcgttttg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttgatg aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatact tacgcctttg
301 agcctgatgt acgacttggc caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt acctatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaaaccaa ttgcagggtt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaaccgc cgcggatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcgat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcttggaac
751 aggatattat ccatggcagg catggaatgg ggcaaatgca cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc ggggtgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAQO
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGRLRLML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDADYM GYGDVKLYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVGR FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

905

```

m582.pep  LNDQRNVYSVLRYNPKTYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g582      LNDQRNVYSVLRYNPKTYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          ||||| |||||
g582      GLMFNDLDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATT:AT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GGCGAAACCG CCGACATCTA TACGCCTTTC
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACACC AGAAACGTGC GGAAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TAAAAACCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAATGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCCGATT AAGGGCAAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYD GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582  100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

551 CCCAATTICA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
g583	MIVDQSQIFT HLAFCFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRI HRARFVGGYAG					
g583	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRI GERTQRI HRARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSRLRDPVGYGQCQNOGAQYCGNGEGY					
g583	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSRLRDPVGYGQCQNOGAQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHD LKKDRPEKSEKX					
g583	RFETQFHHD LKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGCGCA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGCGCGC AAATCATAAC TCGCATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTICA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSRLRDP VGYGQCQNOG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFCFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					

909

m584.pep..

```

1 MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVA EGRDKNVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep      EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK VEGRDFDELN
              ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           EFVKKFNNFTRKSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK AEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADA ALXYTDFHVS RERRNEVIXQ VSKDAV RFKARA EKLAVL GASGYKIVKL
              ||||| :||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           RFIADVQTDASLED TFSVSRERRNEVIDQVSKDAVLRFKARAE VLAGVL GASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              ||: ||||| ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTD SAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCOA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGATTTC CATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
a584           MLRSILAASL----- IVEFS ESAGVEAVQDTMSARFQVTA EGRDKNVNA
              10      20      30      40

```

m585.pcp..

m585 / g585 88.3% identity in 231 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

1	ATGAAACTGT	TCCAACGCAT	CTTCGCCACA	TTTTGCGCGG	TTATCGTCTG
51	TGCAATCTTT	GTGGCGAGTT	TTTCTTTCTG	GCTGGTGCAG	AACACCCTTG
101	CGCAAAACCA	GTTCAACCAA	CGCCGCGACG	TCGAAACAC	TTGTATGGGC
151	AGCATATCGA	CCGCATTCCG	GGCAGCGGGG	GACGCGGGTG	CGCGCGAAAT
201	CCTGACGGAA	TGGAAGACA	GCCCCGTCTC	ATCGGGCGTG	TACGTTATAC
251	AGGGCGACGA	GAAAAAAGAT	ATCCTGCACC	GGTATATCGA	CAGCTACACC
301	ATCGAAGCGG	CCCGGCTTTT	CGCCGCGCGA	CACCCGATT	CCAACCTCGT
351	CCATATCGAA	TACGACCGCT	TCGGCGAAGA	ATACCTGTT	TTCAACCAAG
401	ACTGGGACAA	ACTCCAAGCC	CGCGCGCTGC	CCAGCCCCCT	GTGTATCCCC
451	GGCCTGCCGC	TGCGCTCGAT	TTGGCAGCAA	CTCATCATAT	TGTCCTTCAT
501	CATCATCGTC	GGACTCGCTA	TGGCGTACAT	CTCTGCCCCG	AAACATTGCCA
551	AACCCATCAG	AATCTTAGGC	AACGGCATGG	ACAGGGTGGC	AAACGGAGAA
601	CTTGAAACCC	GTATCTCCCA	ACAGGTCGAC	GACCGCAGAC	ACGAATTGTC

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatatTT
51 ttggaaaacc acgggcaaAT ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccAAA accgtgccgc ttcccaaaAT
151 caggaagcgg cggcgggtgct ggcaaacATc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaATca atgccgaact gtccaaactc caacaaagct
251 acccccatTC catttccgcc gccaagcca cgtgatggc ggccggcaacc
301 gaatttgacg cgcagcgTTa cgaTgttgcc gaaggTcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttggcg gcgcagcgTC
401 tgggcgttGT gttgttgcaa caaaaaaAT acgatgccgc gcttgccgca
451 CTCgacacgc cggttgaggc ggacttcgcc CCCctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggc ttTggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRASQN
51 QEAAAVLANI VEKAQNKAPQ SEINAEISKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLQALA AQLRGVLLQ QKKYDAALAA
151 LPTPVEADFA PLLMETKGDV YAAQKSQEA LKNYGQALEK MPQDSVGRRL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CTGTCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAAATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAAT GACCAAACTC CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGGAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAEITKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLQALA AQLRGVLLQ QKKYDAALAA
151 LPTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGRRL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKT TGKWL <u>FALLI</u> LAALGYLGYT VYQNRKVSQN QEAAAVLANI					

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLK
               |||||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLK
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1   atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggg ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcc accgaaattc aagaaaacgg cagc-atacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgcggcg atcagccaca
401 ctttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKKRGCLP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCCG
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCGCCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAAACCCACG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1   MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGLTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTILSDGIR
201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGH					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGH					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagaagac gggcttcctt caggcaaaag catatggcgt
151 tgcgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgcggc ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag ccttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aacctctctt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCG TTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

```

301 atcgggatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcatgtttg actggcaagc atagtgcac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggg
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcy gcgcacggt
551 tggcgcatgt gtattttgaa gcgggcgtga tggatgatcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cggcaccaca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaaac catcgctgcc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcggcgaa gtgttggcgg gcgcgctgat gaccgaaggg
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaaccc tgcctcggcg
951 catgatgaac gcgtctctcg aagcacaagg cagtaaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggatattg tgccaaactgt cgtgggcate
1051 gcgcttctga cttttatcgt tgcctggctg attaaggggc attggacggg
1101 cgcactgatg cagcccggtg ccgttttggg gatcgctgc ccgtgcgcgc
1151 tcggctctggc gacccctgcc qcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agcgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcagggtgc cgcggtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgcgctcgag caaaacggcg cccaccgct
1401 cgcgcgcgcc atcgtctcgc ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaaac gttgtcggag caggcattac cgcgcaagt
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaattg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttcgga
1601 tatctgtaaa cggcaaacgc atcggcgcat tcgactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tctctatatt atgagcggcg ataaccaaag tacggctgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtcc gtgcgacaaa
1801 gccgcggaag tgcagaaact caaagccgcc ggcaaaacgc tggcgatgg
1851 cggcgacggc atcaacgacg cgcgcgcgct tgcgcgcgcc aacgtcagct
1901 tcgccatgaa aggcgggtgc gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgttaa acggttcgcc gatgcctgc tgatatcga
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttctctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcg caatggcggc aagctcggtt tcggatattg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIARI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPI YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHYFFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPOVAAVY YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFALTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCGGTTCTTT

```

921

```
g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIKI
           10      20      30      40      50      60

           70      80      90      100     1      110
m589.pep   IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||||
g589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTNRHDWMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep   PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      PPVWQFVLASIVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep   AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep   IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep   SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
           |||||:||||| |||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL
           310     320     330     340     350     360
```

923

```

1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CGCCCGAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGTTGCCG
1601 TATCTGTAAG CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAACCG TGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGTTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTGCGCTC GCCGCGCTCG GCTTTTAAA CCCGTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIABI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMMLKG LNWTRHDWML SPLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVHYFE VGIMVIGFVS
201 LGKFEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPCQVAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFALTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEIAGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

10      20      30      40      50      60
m589.pep  MQQKIRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTTSVADIABI
          ||||:|||||
a589      MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTTSVADIABI
          10      20      30      40      50      60

70      80      90      100     1      110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG----RHDWMI
          |||||:|||||
a589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
          70      80      90      100     110     120

120      130      140      150      160      170
m589.pep  PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          || |||||
a589      SPLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130      140      150      160      170      180

180      190      200      210      220      230
m589.pep  AYGMHVHYFEVGMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
          |||||:|||||
a589      AYGMHVHYFEVGIMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
          190      200      210      220      230      240

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925

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501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggc ttcaaaagct
551 accgcaacag ctatgatgcg ccttgtttca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatttc gattcggaag cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggt gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcggggcgcg ttatcgaca gcgaaggcgg gttccgtttc
901 gatacgttgg tgtacggcga tgaataaac ggcgcgctgg acatccatat
951 cgctgccgaa cactcgaatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgcaaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaagg cgaatgcttc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tctcaaaaa atgttggaag atttgccggt aagtcaggct ggaaatatat
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccctaaaaa caacgccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

```

g590.pep.
1 MKKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TG.LLVESHQ
51 YDRGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSYSRNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGKKEDLN
401 QLGLMLKkte ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIA D
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1 ..TGGTTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCTG TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGG AAAATTCTCC CTAGAATGGA
551 AAGAGGTGTG CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCAACGGCA GCATCGCACC
651 TTCCAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGCGAGT TCCGTTTCTG TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCCG TATTGGACAT
951 TAAAACTTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTTGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCTC CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1   ATGAAAAAAC CTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCTG ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGTGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTGCCCAGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTT GATTGCGAAA CTTACAGCGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTCAC GCTGCCATCG GGAATAATCG
1151 ATGTGGGCGG AAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1   MKKPLISVAA ALLGVALGTP YYLGVAEES LTQQQKILQE AGFLTVESHO
51  YERGWFTSTE TTVIRLKP EL LHNQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDKEY GPLDIHIAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQL KLNKGTQLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep
10 20 30
WFTSMETTVIRLKPPELLNNARKYLPDNLKT
|||||

a590 VKAEESLTQQQKILQEAGFLTVESHOYERGWFTSTETTVIRLKPPELLHNQKYL PDNLKT
30 40 50 60 70 80

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
90 100 110 120 130 140

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

929

```

1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO
51 YERGWFTSME TTVIRLKPPE LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PAFDYELSG
201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNNGSIA PSYIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVL DIKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQKL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQX

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAES	LTQQQKILQE	TGFLTVESHO	YERGWFTSME
g590	MKKPLISVAA	ALLGVALGTP	YYLGVKAES	LTQQQKILQE	TGFLTVESHO	YERGWFTSME
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPE	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTVIRLKPPE	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFDYELSG	IRLHWEG	LTGETVYQKG	FKSyrNGYDA	PLFDYELSG
g590	FKSYRNGYDA	PLFDYELSG	IRLHWEG	LTGETVYQKG	FKSyrNGYDA	PLFDYELSG
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSYIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSYIEVGKLA	FSTKTGESGA	FINSEGQFRF
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVL	DIKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
g590	GLFTNNPVL	DIKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRLMVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRLMVD	STVQSMAREK	YLTNGDQID
	490	500	510			
m590-1.pep	TAISLKNQKL	KLNGKTLQNE	PEPDFDEGGM	VSEPQQX		

931

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGc ctcATGGCAG
751 GAATGggcaa acctgACccg cCAA3CCCG ggcAAAAAAA Tcacccgtgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTcAGC
1051 CATATTTCGG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1  LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRK
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDQWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWAQIR RSYRPSVVR AFGMGWKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIR KPLGERVQNI GLRFLALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACCTGCGC CCTACGTCGG CACAGTCGAA CCCGACCA
401 TTGCCGCCCC CGCCGCTTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTcAGC
1051 CATATTTCGG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

933

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAC CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCTTTTAAAA TCACAAACCGT
651 TGCCGGCGGC GTGAAAAAAG GCAGCCCGCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACGT
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAATCCGCG CGCAGCTACC GTCCGCTCTT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGCA
1001 CAACCCCTCAA ATTTTTCGGC AAATAATCA _JGGCAACGC CTCGCTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGCT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKRK
51  DTEWCLAPIP LGGYVKMVDL REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAAPAGF QSGDKIQSVN
151 GTPVADWGSQ QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLGLALM LMMVAFFND VTRL LG*

```

m591/a591 99.6% identity in 446 aa overlap

```

              10      20      30      40      50      60
m591.pep      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKRK DTEWCLAPIP
              |||
a591           LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFETRKRK DTEWCLAPIP
              10      20      30      40      50      60

              70      80      90      100     110     120
m591.pep      LGGYVKMVDL REGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
              |||
a591           LGGYVKMVDL REGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
              70      80      90      100     110     120

              130     140     150     160     170     180
m591.pep      ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGSQAQTEIVLNLEAGKVAVGVQTA
              |||
a591           ELRPYVGTVE PDTIAARAGF QSGDKIQSVNGT PVADWGSQAQTEIVLNLEAGKVAVGVQTA
              130     140     150     160     170     180

              190     200     210     220     230     240
m591.pep      SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
              |||
a591           SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
              190     200     210     220     230     240

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTGCAA ACATGATGA
 101 TGGGCATCAA ACGCGGCTG TATCCAACG AGCGGGTAT GGGTCCGCG
 151 CCGAACGCGC CCGCGCCGC CGAAGTGAAA CACCCTGTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATC CATCATCGTT TGTTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGCGC
 351 GGGCTTCCTC GCCGTCAATC TGTTTATGTT TGCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTGTGCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

```
m593.pep ..
  1 MLELNGLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
  51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPFHMS LENAAGFLKM
101 QKMPKAEAER LAMAALAEVG LENEAHKPKC KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTADD
201 ETAVMHKGRI LQYGTPETLV KTPSCQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GAVSGKDTVR
301 IHIEERIVR FR*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m593.pep	MLELNGLCKRFGNKTVADNICLTVGRGKILAVLGRSGCGKSTLLNIAGIVRPDGGEIWL					
g593	MLELNGLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSGLDTHLRGTLRMRMTAERIRN					
g593	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSGLDTHLRDRLRMRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPPEACTTADEIAVMHKGRILOYGTPETLVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPPEACTTADEIAVMHEGKILOCGTPETLIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

939

```

|||||:|||||:|:|:| |||||:|:| ||||:|||||:|
a593      GGIPAVLVTHSP EEACTAADEI AVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
          190      200      210      220      230      240

          250      260      270      280      290      300
m593.pep  RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLD MRHAGAVSGKDTVR
          |||||:|||||:|:|:| |||||:|:| ||||:|||||:|
a593      RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLD MPHAGEISGNDTVR
          250      260      270      280      290      300

          310
m593.pep  IHIEEREIVRFRX
          ||||:|||||:|
a593      IHIEDREIVRFRX
          310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTTT agcatactcc ggctgctggt ccgcacCGGA attgggatcg
101 gtaagttcgc cgttcaggcc ttTCAGGTCT ttaagctgct gatctGTACG
151 gttgagcacc caaatCGGTT TGCCTTGCCA CTCGCGGTC AGCAGCTGAC
201 ccgcttcgat tttactgaca tccacCTCGA CGGCAGCACC ggaggcCTTG
251 gctTTTTCCG aagggAAAAA actggCCACA aacggCGTTG ccacacCCAA
301 tgctGCCACT ccgcccCGGC CGCAGGTCGC aagtgtCAGG aaacggCGGC
351 ggccgttggt gatTTCTTGA ttatccatta ttcagTCGTC ctaatatTTT
401 gggaatgCCG agccattAAA cattgcaatt ttaccCAGTt tgcagtGATA
451 ctcaaagcat tatttAAAAT aaggtAA

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCC CGC CGCAGGTCGC GAGTGT CAGG AAACGGCGGC
351 GGCCGTGTGT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTtAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap


```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatitggaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cggcaccgcg gtccattacg aacgcacgac accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gtccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaaacagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gtcccgccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa
```

943

```

m595.pep      VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT'
               |||||:|||||
g595          VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRLLPGEYEMTCGLLT
               70      80      90      100     110     120

               130     140     150     160     170     180
m595.pep      NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
               |||||:|||||
g595          NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
               130     140     150     160     170     180

               190     200     210     220     230     240
m595.pep      KAKSLFADTRVHYERIEPIAE LFS ELD PVIDAREDDFKDGA KDAGFTGFHRIEYALWVEK
               |||||:|||||
g595          KAKSLFAATRVHYERIEPIAE LFS ELD PVIDACEDDFKDGA KDAGFTGFHRIEHALWVEK
               190     200     210     220     230     240

               250     260     270     280     290     300
m595.pep      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEVAGSKISGEEDRYSHTD
               |||||:|||||
g595          DVSGVKETA AKLMTDVEALQKEIDALAFPPGKVVGGA SELIEEAAGSKISGEEDRYSHTD
               250     260     270     280     290     300

               310     320     330     340     350     360
m595.pep      LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLG
               |||||:|||||
g595          LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTK DGFETYDKLS
               310     320     330     340     350     360

               370     380     389
m595.pep      EADRKALQASINALAEDLAQLRGILGLKX
               |||||:|||||
g595          EADRKALQAPINALAEDLAQLRGILGLKX
               370     380

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1   ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATAT TAAAAACA CCGGCCCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGCGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1   MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPLGS

```

945

```

451   ttccggcgata aagtgtctgat tgacgggttg agcttcaaag tgcggcgagg
501   cgcgattgtc ggcatcatcg gcccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcca agtgaaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagccgag aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgccccgc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttggcgagg ggcaatgtgt
851   tgctgtctga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgtttga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg ttctctgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaagcg gcgaaaccga aacgcacaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMQKE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GOTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDDEPS NDLDEVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF PDGNYQEYEA
351 DKKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTTC TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 CGCAGAAAC GTTTGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTC GTCCACGGGC GGCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTTC
501 CGGCGGTGAA AAACGCCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTTCG
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCGGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTGA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTGCAAGGTT GGTCAAGTTG AAATCCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTTGC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
g596	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACESDSKWVFFDGN	QEQYEADKKRPLGEEGAKPKRIKYKPVTRX			
g596	ACEGDSKWVFFDGN	QEQYEADKKRRLGKEGAKPKRIKYKPVTRX			
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTTC TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 CGGATATGCT TTTGCTGGAC AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTGTG
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGGAACG GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAG ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAA ACCTGCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTGTG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGTTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNQ QEYEADKKRR LGEEGTPKPR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

g597 . pep

m597.seq

m597.pap

1	MLLHVSNSLR	QLQEEIRIQE	RIRQARGNLA	SVNRKQREAW	DKFQKLNTEL
51	NRLKTEVAAT	KAQISRFVSG	NYKNSQPNVA	ALFLKNIAEPG	QKNRFLRYTR
101	YVNASNREVV	KDLKEQQKAL	AVQEQKINNE	LARLKKIQAQ	VOSLLKKQGV
151	TDAAEQTLEP	RONAKIAKDA	RKLEAQQKNE	QQLNKLLENL	EKKKAEHRIQ
201	DAEAKRKLAS	ARLAAAEKAR	KEAAQQKAEA	RRAEASNMLTA	EDRNIQAPSIV
251	MGIGSADGFS	RMQGRLLKPV	KGAVPTGLFGQ	NRSAGDIWKG	VFYSTATPATV
301	ESIAPGPTVSY	ADELDDGYGV	VVDVHDENYI	SIYAGLSEIS	VGKGVMVAAG
351	SKIGSGSGLP	DGEEGLYLOI	RYOGVGLNYS	SWIR*	

951

```

951  CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGTCGC TGCCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```

1  MLLHVSNSLK QLQEEIRQEI RIRQERIQA RGNLASVNRK QREAWDKFQK
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKTGFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGO VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEEIRQEI RIRQERIQA RGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEEIRQEI RIRQERIQA RGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
a597.pep	70	80	90	100	110	120
	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
a597.pep	130	140	150	160	170	180
	QOKALAVQEQKINNELARLKKIQANVQSLLKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
a597.pep	190	200	210	220	230	240
	QKGNEQQLNKLLSNLEKKKA EHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKA EHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
a597.pep	250	260	270	280	290	300
	SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
a597.pep	310	320	330	340	350	360
	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
a597.pep	370	380	390			
	SGSLPDGEEGLYLQIRYQGOVLNPSSWIRX					
m597	SGSLPDGEEGLYLQIRYQGOVLNPSSWIRX					
	360	370	380			

953

```

      |||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLPRALSMG
      70      80      90      100     110     120

      130     140     150     160     170
m601.pep KLHHAMMCTASVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      |||
g601  KLHHAMMGIASVAI--AAAVLGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCSAA AGTCGCCTTC GTCGCGCCCG CCGCGGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTATGAG CCGCAGCGCA CGCGTGATGA TGGAAAGGTG GGTGAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      |||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      |||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      |||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170     180

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLLGRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TGCCTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGAACGCGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCACGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCCG GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAC
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCC ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GGCACACCGC ATCCGGCGCT ATACAGCTAT
901 CCGACTTTCC ACGCAGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTTCCCGG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCGAG GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATTT CTTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGAAAAAA CGCTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA RYKGIKFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKROVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDPLGL
401 HIDTKANMEK RYNGSGIISP TDSSPAVLVV PTNEELMIAC DTAEIAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```


957

```

g603      LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSND CRTLEIAADEGHEGARLAL EVM TYRLAK
          |||||:||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGIS ELPND CRTLEIAADEGREGARLAL EVM TCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTTCAGACGA CCCACACACC. AAAAAACAAC CACAAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGCG CGGAAGTGCC ACGCCGCGCG
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCAGTCTG CCCAATGTCT GCGTGATGGA TACTTCGTTC
601 CACCAAACCA TGCCCGAGCG TGCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TGCGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCGGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGCGGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCTGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CCGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDDEPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQE""PGL PNVGVMDTSF

```

959

```

251  ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
301  AAATTTTTC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
351  TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAACGGT CGGAATGCCC
401  GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTGGCA CATCAATTC
451  GTCGACCAA TTGCCGTTG GGAACATACT GCCTTcgccg TCGGCTGGAT
501  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604 .pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGFAAG GGVIGGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQGGIVV DVVLQLFARV AQVGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604 .seq

```

1  ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGTACGGCG GCGGCGGTCC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCG TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCGTTCA CGGTTTGCC ACTGGAGGCG GTGTAATCGG
201 CCGCGGGGCG GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAC ACCCATTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTGTATG TCGTCTTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCCGCGT TGATGAGCGT GGCTTTCAA CCGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCG
501 CTGGATC

```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604 .pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVO FAHAQGAYQQ
51  IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFQRTVSAD
101 FLEFFQSRGI VDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604 .pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVOFAHAQGAYQQIDVGGVHGFA					
	: : : : : : : : :					
g604	MPEAHFFTRS AACGKVDQRT EHG--DGDRGDAHHSVVQFAHAQGAYRQIDVGGVYGFA					
	10	20	30	40	50	
	70	80	90	100	110	120
m604 .pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA					
	: : : : : : : : : :					
g604	AGGGVIGGGRDEGDFRRARAGGFGYVADQTHFQRAICADGFKFFQRGIVVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604 .pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI					
	: : : : : : :					
g604	RVAQVGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604 .seq

```

1  ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGCACGGCG GCGGCGGTCC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCATTCA CGGTTTGCC ACTGGAGGCG GTGTAATCGG

```

961

```

951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIEEGFF
251 GQEINHHTYN LARMNMF LHN VNYNKFHIEL GDTLTNP KKLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNLYSGRG
351 RAAIVSFPGI FYRGGAEQK ROYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVL SKHKDNT DIQFIDASGF FKKETNN NVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGACAG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCGGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCTC CAAAGGCGTG GCGGAACTCG ATTTCCGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCTCACTA CGTGCCAAC GCAGGCAAAT CCGGCGCGCA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

	430	440	450	460	470	480
m605.pep	490	500	510			
	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
:	: :	:				
g605	VIDIRQLNAEISSETVAKIERLRREIDEVIAEIETX					
	490	500	510			

a605.seq

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pnp

1	MMTEIQRAQ	LHRQIWKIAD	EVRGAVDGDW	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGYFIYPGQL	FCNIAAEAHQ
101	NEELNFKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLA AVLKGV	AELDFGSFED	HHIDLFGDAY	EYLISNAAAN	AGKSGGEFFT
201	PQSVSHTLIAR	LAVHMGKEVN	KIYDPACGSG	SLLLQAKKQF	DEHIEEGFFT
251	GQEINHYYAN	LARMNMFLHN	VNYNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351	RAAIVSFPGI	FYRGAEQKI	RQYLVEGNVV	ETVIALAPNL	FYGTGIAVNI
401	LVL SKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KDNGYNLAVS	SYVEPEDTRE	IIDIKQLNAE	ISETVAKIER
501	LBREIDEVIA	EIEA*			

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	QLHRQIW	KIAD	EV	RGA	VDG
	WDFK	QYVL	GLT	LFY	RFI	SEN
	FTD	YMQ	AGD	SS	IS	
	:	:	:	:	:	:
a605	MMTEIQQR	QLHRQIW	KIAD	EV	RGA	VDG
	WDFK	QYVL	GLT	LFY	RFI	SEN
	FTD	YMQ	AGD	SS	IS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	II	TP	EIKD	DA	VK
	VG	YFI	YP	GF	NC	NI
	AA	EA	HA	QNE	EL	NT
	KL	KE	IF	TA	ES	SA

965

g606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCT GGTACGATG GTATTCCAAA TCCTGTTCCG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCC GCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGTATC GCCGCGCTCA AATCGCTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

```

601  GGTTCGCGCG TGGCGACAAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651  GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701  CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751  gGcgcgCCCA TCGGGCTGTC TTATTTTGTG GAAgccaGcg cGTTTTCGTT
801  TATCGTGTTC TTGATTGCGC CTttcggCGA GGATTATGTG GCGGCGCAGC
851  AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901  GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951  TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCT GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCCT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTT ATTGCCTCGC
1301 TCACCATCGC AGCCGTGCGC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYA SSLNRPRIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMI PQSV
301 SAGYTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFRSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFIH
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCGCTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCACTCTTC CCTTCCCTT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCACG
251 TTTACGGCGC GGGTAAAACC GACGAAAGTG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGTACACC GCGCGCTGCA CGCTACACT TCCAGCCTGA ACCGCCCCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATC
751 GGCGACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGCAGA CTTACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCATCGCC TTGGTGTGGT GCTTGGAAAT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSF PVFLKEVRLT TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGGTGTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TTAGCCTGA ACCGCCCSCG
501 CCTGATTATG TTGGTCAGCT TTGGCGCGTT TGTGTGAAC GTGCCGTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCCGAT TGGCGGTGTC TCAAACAGAT TTGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GCGCGCAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMFAA
151 MVHRALHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVEFKQIWKI
251 GAPIGLSYFL EASAFSEFIV LIAPFGEDYV AAQQVGISLS GILYMIPOSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFRRSLV
351 SMYNNPDAVL SIAATVLLFA GLFQPAFTQ CIASYALRGY KVTKVPMTFH
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFVPFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVPFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
	190	200	210	220	230	240

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep
 1 MSALLPIINR LILQSPDSRS ELAFAAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGLILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GGFSRESESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng)

from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAFAAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
g608	MSALLPIINRLILQSPDSRSELTSEAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPPAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
g608	TFRNSAIRKILQGGEPPAGDIRLEGLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGKIQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
g608	RATDIGHGKIQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq
 1 ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
 51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
 101 TTGCCGGGTT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
 151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
 201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG
 251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
 301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
 351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
 401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
 451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
 501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep
 1 MSALLPIINR LILQSPDSRS ELAFAAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGLILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GRFSREPESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60


```
a609.seq
  1  ATGGTTGTGG  ATAGACTCGA  AATTCTCGCT  CTCGACGACG  AAACTCTTGA
51  TGCCTTTGTC  GGCAATCAGC  GAAGTAGCGA  CATCGCGCAC  CATATCTTCC
101 ACGAATTTCG  GGTATTTCGT  GGCPTTTTCG  GTAACGTATT  TTTTCATCGG
151 GCGTTTGAGC  AGGCCGTAGA  GTTGGCAGCT  CGCCTGCGCC  TCCACATAAT
201 CGATGACTTC  CTCGATACCG  ACTTCGGCAT  CGGCAGTCAG  GCTGACGGTA
251 ACGTGCGAAC  GCTGTTGTGT  CGCGCCATAT  TGGGAAATTT  CTTTGGAAAC
301 CGGGCAAAGC  GAGGTTACGG  GAATCATGAC  TTTCATACTG  TGGCCGTATG
351 CACCGTCTTT  CATTTGCCCC  GTAGGCTGCA  CATCATAATC  CAGTAA
```

a609.pep
1 MVVDRLEILA LDDETLDFAV GNQRSSDIAH HIFHEFRVTV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLV FALGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HEAREADIII Q*

		10	20	30	40	50	60
m609.pep		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHIFHE
		FRV	FVG	FFGN	VFFI	GA	FEQAV
		ELAA					
a609		MVVDRL	EILALD	DETLD	AFVGNQ	RSSDIA	HHIFHE
		FRV	FVG	FFGN	VFFI	GA	FEQAV
		ELAA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTLVV	RAVLGN
		FFG	TRAKRG	YGNHDL	HTVAV	CPVF	
a609		RLRLHI	IDDFLD	TDFGIG	SQADGN	VRTLVV	RAILGN
		FFG	TRAKRG	YGNHDL	HTVAV	CTVF	
		70	80	90	100	110	120
		130					
m609.pep		DFARET	DIIIXQ				
		:					
a609		HFAREA	DIIIXQ				
		130					

g610.seq

```
1 ATGATTGGAG GGCTTATGCA ATTCTCTTAC CGCAATGTTC CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATATGCTGAC CGCGATGAT TTAGTTTATC CGGTGTTCGT ATTGGAGGGG
151 CGCGGCGCGC AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCCAGAG
201 TTTTGGACAGG TCTGCTTTTA CGCCGAAGA GCGCGTGAGC TCTCGTATTTC
251 CGATGTTGGC ACCTTCTCCC GTGGTTACGG CAAACAAAC CGGGCGCTCC
301 CAGGAGGCGT CCAATCCCCA AGGACTCGTG CCGTCAACTG tccgagcctt
351 GCGCGAGAGG TttCcgaac tggggattat gacgagtgtc ggcctcgAtc
401 cttatacggt gcacGGTCAG GACGGCAGTA CGGACgaaaa cggttACGTG
451 ATGaatATg aaaCCGTAGA AGTCTTGTGT AAACAGAGTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CAGATGATG GACGGGCGTA
551 TCGCGCCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGGCG
601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG AAAGGCAGAT AAAAAAGCCT
701 ATGACATGGA TCTCTGAAAT ACCGATGAGG CGTGCATGTA AGTGCGCTGA
751 CATATTCCAG AAGGTGCGGA TATGGTAGTG GTGAAGGCCG GTTGGCCGTA
```

975

```

g610      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCGTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGTTACGG CAAACAAAAC CGAGCGTGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV LESLLAFKRAG ADGILTYYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPSARMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||
a610      MIGGLMQFPYRNVASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLG LCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          10      20      30      40      50      60
              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          70      80      90      100     110     120
              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
g611          130     140     150     160     170     180

m611.pep      X
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCCG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCTGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTCCGGG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCG AACGGGTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTCCG CGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGF PHQGFARHFL
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLG LCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          10      20      30      40      50      60
              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          70      80      90      100     110     120
              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
a611          130     140     150     160     170     180

m611.pep      X

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||
a612           MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90      100     110     120
m612.pep      KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||
a612           KCAENVLFEEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90      100     110     120

m612.pep      GHSNX
              ||||
a612           GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGAT GCCGTGTCCG ATGTCGGTGG CACGgctgcc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTCgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCTG
301  CCTTCGAGCC TGATGTGCCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGGATTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTATG GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCTG
301  CCTTCGAGCC CGATGTGCCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT

```

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMPASFS	PAMFRVSVLP	AKAASSERLSGLCRIRRLMMG			
g613	LLRKVISVSAKPFPAESKPSSVMPASFS	PAMFRVSVLP	AKAASSERLSGLCRIRRLMMG			
	130	140	150	160	170	180

	190	200
m613.pep	RRADIFSDRGGECLLLLLPLILQAX	
g613	RRADIFSDWGGECLLLLLPLILQAX	
	190	200

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```
a613.seq
1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTTGCGGA  CTCGGGTTCG  CGGGAAATC   TGCCGATTG   TTCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCCTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACCGAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCC
301 CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTGCGGA   AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTCCGAGCG
501 GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTGCT  GTTGACGCTT
601 ATTTTACAGG  CTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```
a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSA
51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSP  DSTAMPRMR
101 PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFP
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*
```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSDS	RENPPICSA	MSAMFLPICLMPCP		
a613	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSDS	RENPPICSA	MSAMFLPICLMPCP		
	10	20	30	40	50	60

	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSS	DARERRLP	SRDSTAMP	PRMRSPSSPMSPAPG	SPPWRIFCTA	
a613	MSAARLPMSACVPKIRANSS	DARERRLP	SRDSTAMP	PRMRSPSSPMSPAPG	SPPWRIFCTA	
	70	80	90	100	110	120

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMPASFS	PAMFRVSVLP	AKAASSERLSGLCRIRRLMMG			
a613	LLRKVISVSAKPFPAESKPSSVMPASFS	PAMFRVSVLP	AKAASSERLSGLCRIRRLMMG			
	130	140	150	160	170	180

	190	200
m613.pep	RRADIFSDRGGECLLLLLPLILQAX	
a613	RRADIFSDRGGECLLLLLTLILQAX	
	190	200

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQOVNNGE VSGVNIIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIIAGEAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD
351  LANLVNEAAL FAGRRNKVKV QSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQOVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIQOVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
g614	PLDDNLIKTL LDKNVRVKVT PEEKPSALTA LFYSLLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRAR LLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRAR LLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIIAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIIAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LANLVNEAAL					
g614	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKV QSDLKTPKT KSIWVRNAAVWX					
g614	FAGRRNKVKV QSDLKTPKT KSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201  TAAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAAC  GCGGCGCGCG  CGGTGtcggC  AACTTTgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGGa  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttctatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTcGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcgggtc  ttCgcgcctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGgtggcC  GATGCCAGG
551 CGCAGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTTCTGT  CgcCGttgc  cgcCGCCGAG  TTTGAATTtG  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTcG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCATTTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTCG  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggCtgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTGATCAA  CAGCGGCGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101 GGCGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKCRLLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAVAAAE  FEFDPsARDV  EFVVDDEDFF  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGAGNFA  EEEFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECGLK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGTGGCGG  CGGTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTCGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151 AGGCGCAGGA  ATTTCCGCC  GCGTGCGGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTGCGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTTCG  CCGGGTGGCC  GATGCCGAGG
551 CGCAGCGGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGCTTTTCAA
601 GCCGTTGTGT  CCGCGGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTcG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAACCAC AATGCGGAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCAGCC ACGTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTGC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGATTTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG TTCCGTA CTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTGCCTGAA TGTCTTTCAA
601 GCGGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCGGGAA GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPGAGNV EFVVDDEDFG GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDFE EEEFFFEK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRVGFSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS	LD	RRRNFP	PRAA		
				:		:
a615	MRKRRRRGVGSFEEQRIDAAAGKPQCGKQAEAVARQLHAASSSSHVWQILD	RRRNLP	PRAA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGTFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGTFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPGAGNVFVVDDEDFGDFELCKR					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPGAGNVFVVDDEDFGDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300


```

551 GAAGCAACCC GCTTCCTGCA CAGCAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTGTC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCGCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCGCGCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

m616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFELG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FOTACSRFPY PNSHDTQAA YPNRIHPRHR RNPRFPALRM QHRRCPLEPR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSQAVAALAQFYKIKPEEILVVHDELDI PCGRIKFELGGGNGGGHNLK					
g616	VWLLKPATFMNRSQAVAALAQFYKIKPEEILVVHDELDI PCGRIKFELGGGNGGGHNLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRRCRQIPASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRRCRQIPAGRTRHHFR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFOTACSRFPYPNSHDTQAAYPNRIHPRHRRNPRFPALRM					
g616	QMGRGNALPAQIIQCRLKPFOTAFSRFPYPNSHRTQAAYPNGIHPRHRRNPRFPVAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCPLEPRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRSTVRRRSGTMRHTCRTRRQIPAPVQNLPNVAGRGGMKLPNRNFSLLSALWFAGG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPPIYRSLMVFALCFAL					
g616	IYSLLFKAADTAPPPFPFHDKAAHLALFFAQILFLAKAFKTKLPPIYRSLIAFAFCFAV					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

g619.seq

g619.pap

m619.seq

1	ATGCCGCTCG	AAAAAAATAT	CGGTTTTATG	GCAGGAAGCA	GCCGCCCGTT
51	TGGGGTGCC	TTTGGCGTGT	TGCTGTTTTC	TCGGCTCCTG	TTTATGACAG
101	TCACAGTCAA	AGGGCGATGG	GATTTTGGTT	TGCAACTCGC	GCTGACCAAAC
151	CTTGCCGCGC	TGCTGATGGT	CGCCTATGCG	GTCGGCGTGT	CCACGCAACT
201	CTTCCAACAG	CTGACCAATA	ATCCGATPCT	GACCCCTTCA	ATTTTGGGTT
251	TCGATTCGCT	GATATGTGTT	TTGACAGACT	TGCTGGTGTG	TACGTTTCGGC
301	GGCGTGGGCT	ATGCTTCCCT	GCCGTTGACG	GGCAAATTCG	GCTTTGAACG
351	GGTGTCTCAT	ATGGGCGCGT	CGCTGCTGCT	GTTCTACACG	CATATCAAAAC
401	AGGCGCGACG	CGAATTTGTC	CGCATGATTT	TAATCGCGGT	GTTCTTCCGGG
451	ATTTTGTGTC	GCAGCCTGTC	GTCGCTGCTT	TCGCGCATGA	TCGATCCCGA
501	AGAATTTACC	CTGGCGCAGG	CGAATATGTT	TGCCGGATTT	AATACCGTCC
551	ACAGCGAGCT	TTTGGGCATA	GGCGCGCTGA	TCTCTGCTGT	CAGCGCGCGC
601	GTCAGTTGTC	GCGAACGCTA	CCGCTTGGAC	GTTTACCTTT	TGGGGCGTGA
651	CCAGGCCGTC	AATTTGGGCA	TCAGCTACAC	CGCGCAACCC	TTTGTGGTAC
701	TGCTTTGGAT	TGCCCGATTG	TGGGCGACGG	CGACCGCGCT	GATCGGACCC
751	GTAAGCTTTT	TCGGGCTTCT	CGCCGCTFCG	CTTGCCAAAC	ACTTTTCCCC
801	GTCGGTCAAA	CATCCGTCCT	GCCTGCCGAT	GACGGTTTGT	ATCGGTGACG
851	TCCTCTTGGT	CGGCGGCACG	ACCGTGTTCG	AACACCTGCT	CCGATGACAG

993

```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCT AACACTTCTT GGGCATGAAG
901 GCGCTATTAA GCGTGGTGGT CGAATTTCG GCGGACTCG TTTTCCTCTA
951 TCTCGTTTTA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGDLPL RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LNHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep      10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
|||||
a619          10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
|||||

m619.pep      70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||
a619          70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||

m619.pep     130     140     150     160     170     180
MGSLLLFYTLIKQGGDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
|||||
a619        130     140     150     160     170     180
MGSLLLFYTLIKQGGDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
|||||

m619.pep     190     200     210     220     230     240
NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
|||||
a619        190     200     210     220     230     240
NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
|||||

m619.pep     250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
|||||
a619        250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
|||||

m619.pep     310     320
AVLSVVVEFAGGLVFLYLVLKHKKKX
|||||
a619        310     320
AVLSVVVEFAGGLVFLYLVLKHKKKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gttttcgccct TAAGTGCCTG
51  CCGGCagggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG CAAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTCA AGTAA

```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTL	LAIVAVSALSACRQAE	EGPPPLPRQISDRSV	GHYCSMNLTEHNGPK	QIFLNGKP	
a620	MKKTL	LAIVAVSALSACRQAE	EGPPPLPRQISDRSV	GHYCSMNLTEHNGPK	QIFLNGKP	
	10	20	30	40	50	60
m620.pep	DQP	VWFSTIKQMF	GYTKLP	EEP	PKGIRVIYV	TDMGNVTDW
a620	DQP	VWFSTIKQMF	GYTKLP	EEP	PKGIRVIYV	TDMGNVTDW
	70	80	90	100	110	120
m620.pep	NP	NADTEWMDAKK	AFYVIDS			
a620	NP	NADTEWMDAKK	AFYVIDS			
	70	80	90	100	110	120
m620.pep	GF	FIGGMGAEDALP	FGNKEQAEKFA	KDKGGKVVGF	DDMPD	TYIFKX
a620	GF	FIGGMGAEDALP	FGNKEQAEKFA	KDKGGKVVGF	DDMPD	TYIFKX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGATT CGATGGTTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAACCC TTTTCCGTTG CTAAAGAAAT CCGTACCGAT
451 ACCGCTGTCT GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGGGAACAG ATTTTTCCTG ACATCGGCGA TTTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCCAGGTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GCGCAGCCAG
751 CTTCCGATAG TCGGCAAGAG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTCATG TTAGCTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACCGT GGACGATATG
901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaaag ccgccgcCgc
951 cgcggaacg ctggTGTCGG AAAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGCAGGCGA GagcgttcCG CTGATTAAAG CCTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAATATGCG ATGAACAGC TTGCCAAAGG
1101 CGcaacCGCG GAAGaggttt TGgaacggct gtccgctCAA CTGACCAACA
1151 AAGTGCTGCA TTCGCCAAT CAAACCTTGA ATAAGCGGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESM AKNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGLDN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCTG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAA CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCGCGA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCCTG CGTCGCTGTC

```

997

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTGCCTGTC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGCTGA TGACGGTTGC CAACCGGAC CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCGG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCGAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGCTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAGAAGAT
1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAATAAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAACLP AVRNLAARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQCGGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

          10      20      30      40      50      60
m622.pep  MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLAARSNAATEAVILSTCNRTELYCVGD
          |||
a622      MQLTAVGLNHQTAPLSIREKLAFAAAACLP AVRNLAARSNAATEAVILSTCNRTELYCVGD
          10      20      30      40      50      60

          70      80      90      100     110     120
m622.pep  SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          |||
a622      SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          70      80      90      100     110     120

          130     140     150     160     170     180
m622.pep  RVAQEQESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          |||
a622      RVAQEQESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          130     140     150     160     170     180
```


1001

```

501  GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGccg actTTCTTcc
551  ggtaTatgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601  ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
  51  FNFEPIAEVG KFLGLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201  TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1  ATGTCCGGCC TTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
  51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
101  CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151  TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201  CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251  CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301  AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351  CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401  CCTTGATGAC GGGTACCCTG TTTCATTCGC TGCTGGCGGT TTCTATGGGT
451  TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501  GGTCRAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551  GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601  ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
  51  FNFEPIAEVG KFLGLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201  TLVFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10      20      30      40      50      60
m627.pep  MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||
g627      MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10      20      30      40      50      60

```

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTCAGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRNTNRPR
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
101 DWIRLRRTFS LNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCTTTAC
101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRPR
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	SDGTSAPAAALQTWILRSVKRLNTNR	PRLKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	SDGTSAPAAALHTWILRSVRRNTNR	PRLKSSAASLMM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRTFSLNFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1005

```

151 VEAVATFVAY EFEMLOMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

```

m629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTTGTC GAACCGTCTGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC
351 CCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGTCT CTGGGCGGTG
551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTTTGC CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGCTGGGC GAAACGGTAA GCGTGAATTT
651 GGGTTTGAAC CCGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTTCGGTCG GCAATATTCC GTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTGCGCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC TCTTTGCTG TTGCTGTGCG
851 ACATTATCGG ACGCGTGATT GTGTTTCCG TCGAAATTCC GGTCTCTACG
901 GTTTTGGTG TATGGGTAC GGCTTTGTTT TTGTGGCTTT TGTGAGGAA
951 ACCCGCCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

```

m629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMTL
101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
151 IEAVATFIAY ENEMLOMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	: : : : : :					
g629	MTAKPFSLNLNLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAAALGLLMTLLLPAAPLPAKMSVAAVAALI					
	: : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLOMLGVWQQGFSSVL					
	: : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLOMLGVWQQGFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	: : : : : :					

1007

```

a629      GMLVFMMILIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccatgt tttacggcat
51  gtacaacgtc GGCGCACAGG CATTCGGTGC CTTAACGCCG GAtttgctgc
101 aacaaagcat cggccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tjtctgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaaagtCTT GTTCGCATCc gtACGCAAAc ACgAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGCGCG TACAGGTAaa AACTTCATGa ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTa CCCCGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAc CGGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCc GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTt GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGa TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggtacat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFA VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NEMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCGCGCAGG CATTCGGTGC GTTAACGCCT GATTTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTGc GACAAATGc TGTTTGGCGC
201 GATTTACTTC CTGCCGATTt ACgCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAc ACgAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGCGCG TACAGGTAaa AACTTCATGa ACCCTGCGCT GGCAGGCCCG
451 GCTTTCCTGT TCTTCGCCTa CCCTGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAc CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCc GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTt GCCCGCATCG
701 CTtcttgGCG CATTATTGCC GGCGTGATGa TCGGTATGAT TGCGATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

```

1009

```

701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTTC GTGCGACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFI VGGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

m630/a630 98.3% identity in 355 aa overlap

          10      20      30      40      50      60
m630.pep  MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQQNIANDWHYAFANALGINMSSEAGVS
          |||
a630      MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQQSIANDWHYALANALGINMSSEAGVL
          10      20      30      40      50      60

          70      80      90      100     110     120
m630.pep  DKMLFGAIYFLPIYATV FVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          |||
a630      GKMLFGAIYFLPIYATV FVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          70      80      90      100     110     120

          130     140     150     160     170     180
m630.pep  ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          |||
a630      ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          130     140     150     160     170     180

          190     200     210     220     230     240
m630.pep  QWAAHGADGLKNAVITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          |||
a630      QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          190     200     210     220     230     240

          250     260     270     280     290     300
m630.pep  GVMIGMIAMSSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
          |||
a630      GVMIGMIAMSSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
          250     260     270     280     290     300

          310     320     330     340     350
m630.pep  YGALIGVMCVLIRVVPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          |||
a630      YGALIGVMCVLIRVVPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTGG TCTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGCGAA ACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCGCAGGA

```

1011

```

m635.pep    MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
a635        MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDA
           10      20      30      40      50      60

           70      80      90      100     110     120
m635.pep    HILKRRGHLILLIQFFXHVLFROLLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRGHLILLIQFFXHVLFROLLPVKIVQKRHRHRSRPAGKIQILLYNIEIAPFFPTLHF
           70      80      90      100     110     120

           130
m635.pep    DFSISNRIIVDX
a635        DFSISNRIIVDX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTGCAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGTCTGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcgggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGGGGCA AAAATTTCGG CAGGTTTTC TCGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGCGGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVGVVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVVFNOG ARGGFFEINT GIHCWQAHTG TGNQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTGCAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGTCTGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TCGGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAGTTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1013

251 GAGKCGIPIS IIDSW*

m638/a635 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLDVNVVNI	GIVDIVEHNALIAAADGD	IVEYFEPLGKHQHI			
a638	MIGGQFIVVGIVGKNALARFVDNVVNI	GIVDIVEHDALVAAADGD	IVKHFEPLGKHQHI			
	10	20	30	40	50	60

	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVGVI	VDGETQIAEAVVFGVVR	AGIGKNAVPPFGNVV	ADDLRTG		
a638	AHIVAHGNIAADFAVVGVI	VDGETQIAEAVVFIGVVR	AGIGKNAVPPFGNIV	ADDLRAG		
	70	80	90	100	110	120

	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRV	ADDFILAHHRIGRTMQI	YADRIIQNIIVFNQ	GARGSF	FEINT	
a638	RVPNGNAIALVHAQSRV	ADDFILPHHRIGRTMQI	DADRIIQNIIVFNQ	GARGSF	FEINT	
	130	140	150	160	170	180

	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAPV	AFDGC	GTVGRPFNRRNFVN	KFGFIYA	
a638	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAPV	SFDGCRTVGRPFNRR	NRFVDVK	FGLIYA	
	190	200	210	220	230	240

	250	260
m638.pep	GSQFERIARPGAGKCGIPISI	IGSX
a638	GSQFERIARPGAGKCGIPISI	IIDSX
	250	260

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCG GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CAGAGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNNIIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101  SDLRFVHYM YTNDSEVSGN ISVGNMGMV LMFSERLKVF DNIavgSRD*
151  GIMLYVNYN DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIMHFTA
201  AIEGTSLDHN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251  FGDSAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV
301  DSKPLMKPYA PKIQTRYQAM KDELLEKET ROSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1015

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTTC GTCCGGCTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CCGCGCCCGC GCGCAGGTCG TCGGCAACGA TATTTCCAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCAATATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGGG TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCGCCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTACGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAA TTTCCCGCCG TTTTGCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GGCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVAVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNVVNY S DIHDNIINKA GKC VFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSWD NSAFDLNGDG
251 FGDSAYRPN G IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQGIMLNVVNYSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQGIMLNVVNYSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSWD					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSWD					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAOFPVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAOFPVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLN					
	310	320	330	340		

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
               |||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFIFKNPPTPSVAPGDIISGATVTL
               130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               |||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
               |||
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||
a640          DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTGCGCGCGC CCGAAATCTG CCTGCCGCGG TATTGCCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG GTTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGCAACGGC
301 GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGCGCgc gTAAGTGTAT
551 TCCGTGGCGa ggTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGGcgac ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTCCGCGC GTTCGTAATC GACGAATCTG

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep			10	20	30	
			ACRRICPLPAISAVQYIFADVVQQEGCGVFVFRLYED			
g642	MRYPFQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADVVQQEGCGVFVFRLLYED					
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFLVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLVFLVQLN					
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEFQLHLRGG					
g642	ACFFFFGGGADELVVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEFQLHLRGG					
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVS					
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS					
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDAVDGVTDGA					
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDAVDGVTDGA					
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVDI					
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDVNGLFVGI					
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGHLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQHQRAFDAGTQP					
	370	380	390	400	410	420
m642.pep	400					
	NGHAVMPRNP					
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

```

a642.seq (partial)
1  GCCTGCCGCC GTATTTGCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAATTCA TGCCTGCTTC
301 TTTTCTTCG CGCGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGTA TTCCGTGGCG AGGTTTTCGA
501 CGATGTTCCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCCCG
601 GATTTCCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```


g643.seq

q643 . pep

m643.seq

m643.pcp

m643/q643

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2067>:

1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644 . pep
 1 MPSERPADCC PVHFVVKFRK LTINCGRFRD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAA^F LKHIESAFRR IFSGDIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNI^FFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPN^DMLY AEIYDQFVRA TAEKEAGIK LDRNQTL^LLDA VQTDVRF^AAV
 451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644 . seq
 1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGCGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC
 201 ATTCGCCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGA GATGATTTC AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
 751 TCCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCGCT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCCGAGA
 1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCTGTGTC CCCCGTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAAATG TGCAAAAAC CTTGGGTGCG AAGGGTTTGG
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
 1251 TGTCGCCGCC ACCGCCGAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCCGCACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCCTGACC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCGCACT CTTTGCTCTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644 . pep
 1 MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAA^F LKHIESAFRR IFSGDIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGRRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI^FFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPN^DMLY AEIYDQFVRA TAEKEAGMK LDRNQTL^LDR LQTDARF^AAV
 451 ARDYTL^PPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644 . pep	MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAA ^F					
g644	MPSERPADCCPVHFVVKFRKLT ^L NCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAA ^F					

1025

```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTAT GCCGAAATTT ACGACCAATT
1251 TGTCGCGGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCGCTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

a644.pep

```

1 MPERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVVXX XXXXEGALVL QPLQEFGEA
151 QIAQGGLDMVF KEGGGGLGVT EPETSGAIA REMQSYEYT DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HVSVPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMLRYPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMLRYPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
	AGHYGVVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGEGLGVTETPETSGAIA					
a644	AGHYGVVXXXXXXEGALVLQPLQEFGEAQIAQGGLDMVFKGEGGLGVTETPETSGAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYTLLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1027

851 TTTCCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```

1  MMMVLALGIS IPVSMMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA
51  SGSRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTL P SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSHA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLK
201 RERLATFTGK SAKRSAKFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

m645.pep	10	20	30	40	50	60
	MMVLALGISIPVSMMVEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
g645	MMVLALGMSMPVSMVEQSNLTNLCCKKSRMTCSSSRSRSCPCATPIRASGSRVSSRSR					
	10	20	30	40	50	60
m645.pep	70	80	90	100	110	120
	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP SLKGLTKVLTARRRLGAVVISEKSRSPSHA					
g645	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP SLNGLTKVFTARRRLGAVVISEKSRSPSSA					
	70	80	90	100	110	120
m645.pep	130	140	150	160	170	180
	ILKVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
g645	MLRVRGIGVAVMVRMSTLARRLSCSFRTPKRCSSSIINKPKFLNFMSSCTNLCVPITI					
	130	140	150	160	170	180
m645.pep	190	200	210	220	230	240
	STVPSAMPSSAALVALLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT					
g645	STVPSAMPSSVALVALLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
m645.pep	250	260	270	280		
	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
g645	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1  ATGATGATGG TGTGGCGTT GGAATGTGCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTGCCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTGGACG
301 GCGAGCGGCG GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGCTTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGAAA TCGGCGAAGC GGTGCGGAAA
651 ATTTTGGCGG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTAAC GCCACAAACG CGGCGCGCAG GGCAGCTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GGCAGGTGCC TGGTCTTCGG
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```

1  MMMVLALGMS IPVSMMVEQS NTLNRCKKKS RMTCSSSRSR SCPCATPMRA

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
g647	MQRLAADGIQIFFVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTGTG TAGGTGTCTGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGT TCGCGATGCT TTGAGCAGGT AATACTSTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTGCGCCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVDDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADERTAHS GGRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : : : :					
a647	VQRLVTHSVQVFFVGVDDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	: : : : : :					
a647	RGAVAVADTVFRQIIRIVDHADERTAHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTGT AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAAAAACA GGTCGGCAGC CGGAATGATA CGCTTGCGTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TCTGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCCGAA ACCTCGTGG GCGAAAAAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAA GATTGACCG CCGCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGTATG CCGGGCTTCA CCGCCCGGA
501 TTTGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1031

```

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

```

a648.pep
  1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
  51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

m648.pep      10      20      30      40      50      60
MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648          10      20      30      40      50      60
MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK

m648.pep      70      80      90     100     110     120
FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648          70      80      90     100     110     120
FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA

m648.pep     130     140     150     160     170     180
FGFDMPQGV E QGCRAAAHAALRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a648         130     140     150     160     170     180
FGFDMPQGV E QGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA

m648.pep     190     200     210
DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX
|||||:|||||:|||||:|||||:|||||:|||||
a648         190     200     210
DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

```

g649.seq
  1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACTGC
  51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCACCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

```

g649.pep
  1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
  51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
 101 FRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

```

m649.seq
  1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
  51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGCGt tcatCCCCAA AAaacaacgc
901 aaacTGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccgTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc ttgcccgcga gaaaccgtcc
1301 gtacgggaac ccgatccccct tgtccgcatt accgaacccg ccctTGCGAC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

g650.pep

```

1 MSKLKTIALT ASGLSVCPGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKPKR
301 KILLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVSI ARIOPAAAOQ ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

m650.seq

```

1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACGGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAG AAACACCCGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCGG
701 TGGGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAACGTCTGC TTCCTGTCCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCCG
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCGA AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

m650.pep

```

1 MSKLKTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KILLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTDYSRN
401 MPAGTVNVGI ARIRPAAAOQ ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1035

```

901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CAAAACCAG CTGTGCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCCGTATT GCCGAACCTG CCCTTGGCAG
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```

1  MSKLKTIALT ASGLSVCPGF LYAQTSSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGFRMGEV NPELVRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNVVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNRYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRCTPCD
451 SRSATSNRKT DRHAV*

```

m650/a650 99.1% identity in 465 aa overlap

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQTSSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
a650	MSKLKTIALTASGLSVCPGFLYAQTSSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFRMGEVNPPELVRRHESKFIASHSYFN RVINRSRPFYHIANEVKKRNMPAEALLP					
a650	LRQGFRMGEVNPPELVRRHESKFIASHSYFN RVINRSRPFYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIIYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAA					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNRYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNRYRSNMPAGTVNVGIARIRPAAQT					

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```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDPMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60
g652          MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120
g652          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDSKGFPTTVGDEGGFAPNLN

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180
g652          SHKEALQLMVEAEEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE

              190     200     210     220     230     240
m652.pep      GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240
g652          GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGKVVQLVGDDLFVTNPKILAEGIEKGVANA

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTSLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300
g652          LLVKVNQIGTSLSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS

              310     320     330
m652.pep      RSDPMAYNQ LLRIEELAE AADYPSKAAF YQLGKX
              310     320     330
g652          RSDPMAYNQ LLRIEELAE AAYYPGKAAF YQLGKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAACAACAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCGTCCGCGT TTACCGCTAC TTGGGCGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GCGGAAGACG TATTATTCGC ATTGGAAGTC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCT CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGGCAAAG TCCAACTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAAAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CACGTAATG AGCCACCGCT CCGCGGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGGACT ACCCCAGCAA AGCCGCATTG TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGA SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCGCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTTC GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGCGTGGCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGCGC TACAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAA
951 CAATCCAAAA ATCTTGGCGC AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLESVMGRAAVPSGASTGQKEALELRDGDKSRY					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLESVMGRAAVPSGASTGQKEALELRDGDKSRY					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

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```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

              70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

              130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR
              130     140     150     160     170     180

              190     200     210     220     230     240
m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPFIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPFIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

              310     320     330     340     350     360
m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

              370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK
              370     380     390     400     410     420

              429
m652-1      AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaagc atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TtgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTgG ttACgaaGTc GCAGaAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTtgacggT GATGTGCGCt TTGCCCCAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG

```

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130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```

g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTTCTTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCCG
301 TTGGCAAGGT CTTCCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCCGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```

g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLT3PV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```

m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCCGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTTCGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACCTTGAC
201 TTCGCCGGTT TTACTIONGATGC GGCCGACGTC GTTGGCGTCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCCG
301 TTGGCAAGGT CTTCCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTTCCG TCGGACGAGG ATTTCCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT C3TAG

```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```

m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLRSRTR ISGEEPTMWK SPKS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRPSTLETMCITWEYFSIT			
	: : :	: :	: :	: :	: :	: :
g656	MPRFSGSISSMISIARTFGA	PESVPAGKVAARMSILVTPS	FKQPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	: :	: :	: :	: :	: :	: :
g656	ILSVTLTSPVLLMRPTSLRP	KSIISITCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRTRISGEEPTMWK	SPKSX				
	: :					
g656	MTSSRSRTRISGEEPTMWK	SPKSX				
	130	140				

1045

g657.ppe

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYGVV

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLP LQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLP LQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51  CGGACAATTA GGCAGAATGT TTA CTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATT CAGGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGCTC GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATT CACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GCGCGACGCT TTGGCCGATG AATTGAAC TA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTC AA
801 CGAAATCGCG CGCGGTCCGC ACAATTCCGG CCACCATACC GTCGACGCTT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGGCCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGGCGACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESI QF LPGLKATATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSXL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAFAAE	FADRHLCAPFDN

1049

```

101 NAIHAAVFGK RGFEFVQREF ADLTFVVAQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVGD
201 VFKEGRRRA FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
  1 ATGGTGTCG GAATTGTGCG GCGCGGGGC GATTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCGGTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTCAAA
251 CCGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGA CCTTTGCCGT CGTAGCCAA CGTAGCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGGTCGGC AAATTCTGCT
701 GCCGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTA
```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
  1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVVAQ RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKEGRRRA FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVG	TQSRGDDG				
g658	MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHVG	TQPRGDDG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDYG	NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY				
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQREF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVVAQRSRFQDAGQKL	RACFSDVFSLTNHLIRRGLQSRFAYPCLFLNAVLCNRHT				
g658	ADLTFVVAQRSRFQDAGQKL	RACFSNVFGLANRLIRRGLQACFAYPRFFLNAVLCNGHA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKEGRRRAFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG					
g658	VAAGGNVGM LQRAHRVGDVFKEGRRRAFCQFVQRPVVKRRAQMAVGKFRRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFGGNGKHSAX					

```

g661.seq
1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGA AAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 ccgccc aaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGcg
401 TACCCGTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GCGgcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CGGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATT TCGCGAACAC GGCGTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCATTTT GAACCATATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGGCGAAAT GCGCGACGGC GAACAGGCGC GGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRAARRARQ AVVFPFREAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCCGCG
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTAC CCTCAAAACC CGTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TCGCGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCAGCGGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCATATC CGCGCCATAC
801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCGCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHDDQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPFETL CRTRCFACIL
251 EFGRMRRRYF EPHPRHTRVL RRHRCARHT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 98.5% identity in 295 aa overlap

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRILCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCARHTQTHRLVHRRNARRRTDTSX
           |||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCARHTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTC CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGTctGC CAAATGCCTG AAATCGCTGG TGGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGCG GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAGC AGTGGCCGCT
551 TCCTGTATCT GCCCGATCAG GATTTGCGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTG GCTGCACAAG CGTTTCAAAA
851 CCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRRNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLO FYPAWKSFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

```

1055

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151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTTCAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGCGGTTTG AATTCACCTG TGCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACCTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGCGTG CGCGCCCTCG TCAAACAGTT CGGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT ACCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTGC
601 GATTTCCTCG GTATTTCGGC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCTGTGC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTGCGGAATC CTTTCCGAGT
751 GAAGATCGCG AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIRRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
a663	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
a663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
a663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIRRTATITGLSRIAALA	NAKVIPAIPVREADNTVTLH				
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK	RFKTRPEGSPDFYX				
a663	250	260	270	280	290	
	FYPAWESFPEDAQADAQRMNRFIEERVREHPEQYFWLHK	RFKTRPEGSPDFYX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAAGC GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGTGAGcgg gGCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAG TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCCaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gttTTTTCaa cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT

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1057

```

201 GGAACACGGT CAACCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTCCTCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGATAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPPHFRAF FINGHGVEIV HLLISGGAHR MCGRTC VFGE LVLAQQADV F
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

          10      20      30      40      50      60
m664.pep  VIHPHYFRAFFINGHGVEIVHLLIAGG  HRMGGRA CVFGE LVLAQQADV DAAHGAAGAV
          |||||:|||||:|||||:|||||  ||:|||||:|||||:|||||
a664       VIHPPHFRAFFINGHGVEIVHLLISGGAHRMCGRTC VFGE LVLAQQADV DTAHGAAGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m664.pep  AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVVGKDELG
          |||||:|||||:|||||:|||||:|||||:|||||
a664       AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
          70      80      90      100     110     120

          130     140     150     160     170     180
m664.pep  VKDVQTLVFHRAHIEIAHGDH ENIQVVFQTEARFVPFHRVFX TIPQRSR PWACPLRWCK
          |||||:|||||:|||||:|||||:|||||:|||||
a664       VKDVQTLVFHRT HIEIAHGDH ENIQVVFQTEARFVPLHC VFXAIPRQSR PWACPLRWCK
          130     140     150     160     170     180

m664.pep  TRFX
          ||||
a664       TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG acgaaacgGg cticgGgttg GAAatgact tggatatttT
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGG CATTGAATCC GTGGTCGGAC ACGAATATT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGCCG GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaaag CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTTCA GTTAACCATT AAACAAACCG
701 TGCCGCCACG GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAAACG GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTCCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```

```

1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGGC CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTGCGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCACAAA
1651 GCCCGTTCGC TCATCGGCAG GTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAAGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
1  MKWDETRFGL EYDLDFIMVV AVGDFNMGMAM ENKGLNIFNT KFVLADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPPPTDM TDKQPMMPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHSDAFTF WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGLEYDLDFIMVVAVGDFNMGMAMENKGLNIFNTKFVLADSRATDTDFEGIES					
g665	MKWDETRFGLEYDLDFIMVVAVGDFNMGMAMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGKLYFORHDG					
g665	PEDAGPTAHPVRPVSYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGKLYFORHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMMPVVKVGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPVVKVGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1061

```

1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCCGC CTGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
1  MKWDETRFGL EYOLDIFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEGFQKGM MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPPTDM ADKQPMMPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHDSDAFTR WEAQAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

m665/a665 97.3% identity in 638 aa overlap

```

m665.pep      10      20      30      40      50      60
MKWDETRFGLEYDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES
a665          10      20      30      40      50      60
MKWDETRFGLEYDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES

m665.pep      70      80      90     100     110     120
VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
a665          70      80      90     100     110     120
VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF

m665.pep     130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
a665         130     140     150     160     170     180
PEDAGPTAHPVRPARYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG

m665.pep     190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM
a665         190     200     210     220     230     240
QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPPPTDM

m665.pep     250     260     270     280     290     300
TDKQPMMPVVKVGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLR
a665         250     260     270     280     290     300
ADKQPMMPVVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR

m665.pep     310     320     330     340     350     360
GFSAPVHLNYPYSDDDLLL LAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK
a665         310     320     330     340     350     360
GFSAPVHLNYPYSDDDLLL LAHDSDAFTRWEAAQTLYRRAVAANLAALS DGVELPKHEK

```

```

1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAAGTG TGGACGGCA CGAAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGCGCGAAG CAGGAAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCGGAC CCGCGGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGGGCAA CTGCCTGTGT GCGCAGTTTG
2201 CGGACAAAGT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCCGCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pap

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWEDTRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNQFP
351 EDAGPTAHPV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIN QTVPPPTDMA DRQPMMPVK VGLLNNGEA VAFDYQGRRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHJSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVIDS
601 DLLDNFAKAL LLGVPSAEAL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLNR VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTLQHP KFSLENPNKA RSLIGSFSRN VPHFAQDGS
801 GYRFIADKVI EIDRFNPOVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCC
101 TGAAGTCGCG TTTGACGTT GAGCCGAGA GGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCTAAGT CACCACCACC ATCGTCGCGC ACAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCGC GGGCGATTGG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACGGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCTCGGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAA ATCCGCTGCG TCGCCAGCA CCAGTTCGCC
1051 GAAGACGCG GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAATAAGGC GCGGAAGTAG
1151 TCGCGGATGTA TCACACCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGTACAG CCAGCGGGC ACGCCGTTT TGAAGCGGA AGGTCTCTG
1351 AAAACATAA TTTTCGAGTT GACCGTCAA CAAACCGTGC CGCCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ACTATCAGG CAAACGCGCG

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1065

	250	260	270	280	290	300
	310	320	330	340	350	360
m665-1.pep	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRRIENIRLLRQHQFEDAGPTAHPV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665-1.pep	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665-1.pep	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPMDTKQPMMPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPMDTKQPMMPVK					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665-1.pep	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665-1.pep	YSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVANLATLSDGVL LPKHEKLLAAVEKVISO					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVANLAALSDGIGLPKHEKLLAAVEKVISO					
	550	560	570	580	590	600
	610	620	630	640	650	660
m665-1.pep	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNROAAK					
g665-1	DLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDROAAK					
	610	620	630	640	650	660
	670	680	690	700	710	720
m665-1.pep	QENQSYEYSPAAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
	730	740	750	760	770	780
m665-1.pep	NESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
	790	800	810	820	830	840
m665-1.pep	RSLIGSFNRNVPFHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFNRNVPFHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
	850	860				
m665-1.pep	VKQALQIRIRAQEGLSKDVGEIVGKILD					
g665-1	VKQELQIRIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTTGATAT TAACGAACCG CAAACCATTTG
101 TGAAGTCGCG TTTGACGGTC  GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT  CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG  AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG  GAAACCGAAA TCCTGCCGGC GAAAAACAAA
301 TCGTGATGCG GGCTGTATGC  GTCCGCCGGT AACCTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA  TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC  ATCGTCGGCG ACAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA  AATCGACGGC GGCGAGTATT CAGACGTCGG

```

a665-1.pep KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
|||||
m665-1 KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
70 80 90 100 110 120

a665-1.pep 130 140 150 160 170 180
FRKITFYIDRPDVMKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
|||||
m665-1 FRKITFYIDRPDVMKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFSKPS
130 140 150 160 170 180

a665-1.pep 190 200 210 220 230 240
YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTADKPKVGF AVESLKNAMKWDETRFGLF
|||||
m665-1 YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTADKPKVGF AVESLKNAMKWDETRFGLF
190 200 210 220 230 240

a665-1.pep 250 260 270 280 290 300
YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATD TDFEGIESVVGHEYFHNWT
|||||
m665-1 YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATD TDFEGIESVVGHEYFHNWT
250 260 270 280 290 300

a665-1.pep 310 320 330 340 350 360
GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIEN IRLRQHQPEDAGPTAHPV
|||||
m665-1 GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIEN IRLRQHQPEDAGPTAHPV
310 320 330 340 350 360

a665-1.pep 370 380 390 400 410 420
RPARYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
|||
m665-1 RPARYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
370 380 390 400 410 420

a665-1.pep 430 440 450 460 470 480
MVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTV PPTPDMAKQPMMPVK
|:|
m665-1 MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTV PPTPDMTDKQPMMPVK
430 440 450 460 470 480

a665-1.pep 490 500 510 520 530 540
IGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVP SLLRGFSAPVHLNYP
:|
m665-1 VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVP SLLRGFSAPVHLNYP
490 500 510 520 530 540

a665-1.pep 550 560 570 580 590 600
YSDDDLLLLLAHDSDAFTRWEAAQTLYRRVAANLAALSDGV ELPKHEKLLAAVEKVISD
|
m665-1 YSDDDLLLLLAHDSDAFTRWEAAQTLYRRVAANLATLSDGV ELPKHEKLLAAVEKVISD
550 560 570 580 590 600

a665-1.pep 610 620 630 640 650 660
DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLD ILAVRFLPKWHELNQAAK
|
m665-1 DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLD ILAVHFLPKWHELNQAAK
610 620 630 640 650 660

a665-1.pep 670 680 690 700 710 720
QENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEKYAE MAQNMTHEWGILSAVNG
|
m665-1 QENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEKYGE MAQNMTHEWGILSAVNG
670 680 690 700 710 720

a665-1.pep 730 740 750 760 770 780
NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQ QVQTALQHPKFSLENPNKA
|
m665-1 NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQ QVVRTALQHPKFSLENPNKA
730 740 750 760 770 780

a665-1.pep 790 800 810 820 830 840
RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAAR LVQAFNLCNKLEPHRKNL
|
m665-1 RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAAR LVQAFNLCNKLEPHRKNL

1069

```

g666      HVTGLTEQKQVIA SDFIVASANPLATQAGYDILKQGGSAADAMVAVQTTL SLVEPQSSGL
           70          80          90          100         110         120

           130         140         150         160         170         180
m666.pep  GGGAFVLYWDNTAKTLTTFDGR ETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLSL
           |||||
g666      GGGAFVLYWDNTAKTLTTFDGR ETAPMRATPELFLDKDGXPLKFMEAVV--ARXVRLSL
           130         140         150         160         170

m666.pep  NX
           ||
g666      NX
           180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2175>:

```
a666.seq
1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTGGC
51  TAA AACATCAT  TTATTGACTG  CATTGTATAAT  GTCTATGACA  ATCTCTGGAT
101 GTCAAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAAATACTCA  TTCTGCTGTC
151 ATCACAGGTG  CAGACGCTCA  CACGCCTGAA  CATGCAACGG  GACTGACCGA
201 ACAAAAGCAG  GTCATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251 TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGCGCG  TAGCGCTGCA
301 GATGCCATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351 GTCAGGCTTG  GCGGCTGGTG  CATTGTGTGT  GTATTGGGAT  AATACCGCCA
401 AAACATTGAC  CATATTGTAT  GGGCGTGACA  CGGCACCCAT  GCGTGCACAG
451 CCGGAATTAT  TTTTGGATAA  AGATGGTGAA  CCATTGAAAT  TTATGGAAGC
501 GGTGGTCTGG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2176; ORF 666.a>:

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSM</u> T	<u>ISGCQVI</u> HAN	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	<u>V</u> IASDFMVAS	ANPLATQAGY	DILKQGSAA
101	DAMVAQVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTE	GRETAPMRAT
151	PELFLLDKDQG	PLKFMEAVVV	VARVRRLLSL	N*	

m666/a666 100.0% identity in 181 aa overlap

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTISGCQVI	HANQGKVNTHSAVIT	GADAHTPE	
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTISGCQVI	HANQGKVNTHSAVIT	GADAHTPE	
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVI	ASDFMVASANPLATQ	AGYDILKQGGSAADAMVAVQ	TTL	SLVEPQSSGL	
a666		HATGLTEQKQVI	ASDFMVASANPLATQ	AGYDILKQGGSAADAMVAVQ	TTL	SLVEPQSSGL	
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKT	LTTFDGR	ETAPMRATPELFLDKD	GQPLKFMEAVVVVARWVRL	LSL	
a666		GGGAFVLYWDNTAKT	LTTFDGR	ETAPMRATPELFLDKD	GQPLKFMEAVVVVARWVRL	LSL	
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

```
a667.seq
1  ATGCGGTTTG  TCTTCTGTTT  GGGCGGAGAG  ATAGTTTCTG  ATCCGCTTGA
51  TTTCATTTCT  GTATTTCGTCT  GCGTCGAATC  TCGCGCTGAC  CAGACAGAA5
101 CGCAGATACA  TCAGATAGGT  ATTTACCGCA  TCGGTTTCGC  AATAATTCGC
151 GATTTCTTTC  AGCCTGCCCG  CGTGGAAACG  CTCCCACACC  TTGCTGCCGT
201 CCATACCCAG  CTTGCCCGGA  AAACCGCACA  GTTTCGCCAT  ATCGTCCAAC
251 GGCACATTTC  CCTTCGGCTG  GTAAAGCGCG  AGCAATCCCA  TCAATCGCA
301 ATGACGTTGG  TGGTAGCGGC  TGATGTAGTT  GTTCCACTTG  AAATCGCGGC
351 TGTGCGCGAC  ATGCGCGCTG  CCCATATCCC  AATAGCGCGC  GGCCTGTGAT
401 CCGTGTAGCA  GCGAAGCGTA  ATCAGAAACC  GGCAGGTGCA  AACCGCGCC6
451 GTTCCAACCT  ACCAGTTGCG  GCGTATGTTT  TTCAATCAAC  TCGAAAAATT
501 TGGCGATAAC  CACTTCTCTG  CCGTATCCCA  TCTCGCCGAT  TGTACCGACA
551 TGGACTTTAT  CCTGCCCCCA  ACGCATGCGA  CAGGAAATCG  CCACAATCTG
601 ATGAAGATGA  TGCTGCATAA  AATCCCCACC  CGTCTGAGCA  CGCGCTTTT7
651 GCTGGGCAAA  CAGCACCCTT  TCATCGTCCG  GCAGCGAGGA  CGGCAAGTCA
701 TACAGCGTAC  GGATACACTG  CACATCGGGT  ACGGTTTCAA  TATCGAAAGC
751 CAAAATCGTG  GTCATGACAG  CACCTTGAT  TTAAAA.CAG  ACTTGCGCCT
801 ATTGTGTCAT  TAA
```

```
a667.pap
1  MRFVFLGGE  IVSDPLDFHF  VFVCVESAAD  QTETQIHQIG  IYRIGFAIIA
51  DFLQPARVER  LPHLAAVHTQ  LARKTAQFRH  IVQRHIRPRL  VKREQIHQIA
101 MTLVVAAADV  VPLEIAAAVE  IAVAHIPIAR  GVDV*QRTV  MQNRQVETAA
151 VPTDQLRRMF  FNQLEKFGDN  HFLAVIHLAD  CTMDFILPP  THAARNRHLN
201 MKMMLHKIPT  RLSTAFLLGK  QHHFIVGQRG  RQVIQRTDTL  HIGYGFNIES
251 QNRGHDSTLY  LKXDRLLLCH  *
```

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPFDHFVVRIPAADQTETQVHQISVCRVGFATIADFLQPAMEC
             |:| :|:: |:|||||| :: |||||||:|:: |:|||||||||||:|
a667        MRFVFCLGGEIVSDPLDHFHVFCVESAADQTETQIHQIGIYRIGFAITADFLOPARVER
              10      20      30      40      50      60

              70      80      90     100     110     120
m667.pep    LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAVAE
             |:|:|||||||||:|||||: |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
a667        LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAAADVVPLEIAAVAE

```

1073

```

m669.pep      FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               |||||:|||||
g669          FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHEH DRSLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

               10      20      30      40      50      60
m669.pep      MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHEHSSLRQHGIEGMGFDFKQI
               |||||:|||||
a669          MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHEHDSLRQHGIEGMGFDFKQI
               10      20      30      40      50      60

               70      80      90      100
m669.pep      FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               |||||:|||||
a669          FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGTCT TGGGCGCGT TCGTGTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC GCGCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTVC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGTCT TGGGCGCGT TCGTGTTCG GGTGGTGAAA
51 AAACGCTTCG GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTCGTCA AACAACTTA

```

1075

```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
a670        FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
a670        SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCCAAATG CGGTTGGCAA AGCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETHHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCCAAA
201 GGCGAGGTGCG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETHHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
g671        MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKKETHHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRFQ NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKAKVAEFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTCTGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCGGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCGGTC CGCATCACCG GAGCGGAATC GGTGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRFQ DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAEFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYQSPRAI	DIIKAQKIAA	ALPPFVSVVA
	70	80	90	100	110	120
m672.pep	LFNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRFQ
g672	LFNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRFQ
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	190	200	209			
m672.pep	SGGVEASKGK	KDAAKVAEFI	ATANRLSRX			
g672	SGGVEASKGK	KDKAKVAEFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVVVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGCGGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTGTGTT
451 GCCCAAGTGC GCGCGGAATT TGAATTTGCG GCGCGGAGG CGGTGAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVVVVEAMR LTDADRVVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

m673.pep      10      20      30      40      50      60
MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
|||||
g673          10      20      30      40      50      60
MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI

m673.pep      70      80      90     100     110     120
YDDTAQFVFVDTPGFQTDHRNALNDRNLQNVTEALGGVDVVVVVEAMRFTDADRVVLK
|||||

```

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TCGCGCAGAG TATATCCGAC AAATCCGCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCaaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151  gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201  CTCTTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTg
51	ggAAACGGTG	CGCTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGGC	CTTCGGGCGT
151	GTTCAAAACC	ACTTCGTGCG	CTTCGCGCGC	TTTAATCAGG	CAACGCGCCA
201	ACGGCGAAAT	CCAAGAAATT	TTGTTTGGCG	CGGTATCGAT	TTCATCGACG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCGCGCCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAATACTT	GGTCGGTTCG	TTTCGCGCAAT	TCGGGATCGA
351	CGACGACGGC	AGCCTCCAAA	CGTTTGGTCA	GGAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGA	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCGCCCG	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTGAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TTCCGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep

1	MPQILVRIFL	IRYSFIWETV	RLCRFRHRHSR	SVDFDVFDK	DFNFLTAFR
51	VQNHVFAR	FNQATRRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQTD
101	GRAEKYLVR	FAQFGIDDDG	SLQTFGOETD	AAVDFAHTAF	AVKIVAVFAA
151	VAVACRPVDD	LDDFGAFFID	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGCTTTTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCGGGCGT
151	GTTCAAAACC	ACTTCGTGCG	CTTCGCGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTGGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGTCGCGCA	ACAGTCGGAC
301	CGTCGCGCCG	AAAACACTT	GGTCGGTTCG	TTTCGCGCAAT	TCGGGATCGA
351	CGACGACGGC	AGCCTCCAAA	CGTTTGGTCA	GGAACGGAT	GCGGCGGTTCG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGA	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCGCCCG	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTGTGAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTTTGGT	TTCCGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep

1	MPQILVRIFL	IRYSFIWETA	RFCRFRHRHSR	SVDFDVFDK	DFNFLTPFR
---	------------	------------	-------------	-----------	-----------

1087

```

m677.pep      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRAEKHLVGRFAQFGIDDDG
                |||||
a677           FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDGRAEKHLVGRFAQFGINDDG
                70      80      90      100     110     120

                130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
                ::|||
a677           GFQTLGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
                130     140     150     160     170     180

                190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
                |||||
a677           PSGGRNVVFGFGTHIVCGX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCGC TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcgcgACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTcATTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACCGGC GCAGTTTCGG CGGTcGGTCT GGGCTTTGCC
301 AACCGcATTt TGGGCGGTGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCGC TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTcGTTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACCAGC GCAGTTTCGG CGGTcGGTtT GGGCTTTGCC
301 AACCGcATTt TGGGCGGCGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTs AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1089

```

151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201  AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301  GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGSTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTGC
451  TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501  TTCGGCTTTG TTTAAACTGA TGTTTTCTG TTTCACATGG TCGAGCAGCC
551  GTCCGACGGT GCGCAGCACT ATTTGCGAGC CGGCACGCAG GTCGGCGGTT
601  TGTTTGTTCA TGTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651  GTTTTAAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1  MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQKTI TWFIKRSTIS RSSRLRFWKV STAMMCCSTL
101  ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SINPISNMRS ASSRTTISAL FKLMFFCFTW SSSRPTVATT ISQPARRSAV
201  CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1  ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51  GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101  GCGCGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201  GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301  GCGTTGGTGG TGTTTTGGCG GGCGACTTCG ACGSTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTGC
451  TCGATAAAAC CCATATCCAG CATAAGGTCG GCTTCGTCCA AAACGACGAT
501  TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551  GTCCGACGGT GCGCAGCAGC ATTTGCGAGC CGGCACGCAG GTCGGCGGTC
601  TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651  GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1  MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQNTM TWFIKSTIS RSSRLRF*MV STAMMCCSTL
101  ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201  CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680       MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90     100     110     120
m680.pep  TLCLVLQNTMTWFIKSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||
g680       TLCLVLQKTTWFIKRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90     100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGSGTGC GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGTCGGT
451  GTATTTCGTCG GTTTCGTTCG CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGCGGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCGCCGCT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

m681.pep
  1  MTTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECLKVSVL
101  RLPVNGLEEC AVFGKLPRAA FGLGKQCGGF RVFGFDVGEA DDAEVVGVVG
151  VFVGVFAAEE TPAAVVFKNK GFAVEADGP VLFGDVGVDG AAVECRGKCL
201  CKCVHCGNTL GGGKLADEFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251  KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
  1  ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTCGG AAGAGGCAAA
 51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101  TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ATGCGCTGCC TTCGGGTTGG GAGAGCTJTG CGGCGGTTTC AGGGTTGGTT
401  TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCCGT
451  GTATTTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501  CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGCGGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651  TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAA
701  TGCGCGCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751  CGCATTCGGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
  1  MTTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECLKVSVL
101  RLPVGDGLEC AVFGKLPCAA FGLGKQCGGF RVFGFDVGEA DDAEVVRIVG
151  VFVGLVAAEE TPAAVVFKNK GFAVEEADGP VLFGDVGVDG TAVECRGKCL
201  CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251  RIRAVFCGRR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

m681.pep      10      20      30      40      50      60
               MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
               |||
g681          10      20      30      40      50      60
               MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV

```

1093

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	GNTLGXKLTDFTT	IRALSADGGGLV	VCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVH	CGNTXGGKLADF	TTILALSADGGGL	VVCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTGTATG GCAGGATTTA TTCGCTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT.....GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTCCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY..EMAMPSEP DWIQTAFCA YGFIRFPTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIC NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..
 1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
 201 TGTACCAAT CTAACAACAG AACGTTTTCG CAACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTGCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

m683.pep	10	20	30	40	50	60
	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGLM					
g683						
	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGLM					
	10	20	30	40	50	60
m683.pep	70	80	90	100	110	120
	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683						
	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	130	140				
	SSLRPMISLSGTLTEKQYETVCGKKLX					
g683						
	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq
 1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
 201 TGTACCAAT CTAACAACAG AACGTTTTCG CNACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTGCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL

151 GYAAMTAALE QGLKQAAQQM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
g684	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
g684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALQGLKQAAQQMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALQGLKQAAQQMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTGG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTGTTTCCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCCTCAT	CAGCGGTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGG	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQQM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
a684	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
a684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

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1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPOLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ LKAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep    LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
g685        LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep    VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685        VSAASQAASTPVATLTVPARGDAVVPKNPERVAVYDWAALDTLTPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep    DYLPQAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAEAYEQ LAKNATTIDLTVDNGN
g685        DYLPQAFDKAATVGTLEFDPCESLHRHNPQFVITGGPGAEAYEQ LAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep    IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRGVLVSVTGNKVSAGF
g685        IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep    TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
g685        TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPGWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep    VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFKKAEPVAAGKKX
g685        VEVLDNALVCGTNWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGGCGCGTGG TTTCTGCAGG
51 TCGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCGCCCC AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGCGGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGGCGGTGGA
351 TTATTGTCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 ACGCAAAGGA CGCGGGCTGG TGCTGTCTGG TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```


This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IIVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TCCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCC ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGGC TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGCGCGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTCTGA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
 451 TCCGTCAACG GGACTACCGG CTTATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAAVLVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
 151 SVNNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

				10	20	30
g686.pep				NFSCRADDVFDDICSAVEGF	GGIARSVQLG	
m686	LKKFVLGGIAALVLAACG	GSEGGSGAXX	XXNFSCSADDVFNDICSAVEGF	GGIARSVQLG		
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAG	IIVETVGKPLSGAAVVGQVEA	DILGNAFYVVAVYIPRAFGS		
m686		AVSGGAFESVAYSLRQHTTG	IIVETVGKPLSGAAVVGQVEA	DILGNAFYVVAVYIPRAFGS		
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFVSV	PMDAVKAESVNGTTGFVRIGMX			
m686		GIAAALWPVIAVGGMVFVSV	PMDAVKAKSVNGTTGFIRIGMX			
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
 151 ATTGTGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTGCGTCA
 201 GGTTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC TAATGGATG CGGTAAAGCG
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

This corresponds to the amino acid sequence <SEO ID 2282; ORF 687>:

```
m687.pap
1  MKSRHRLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
5  TVLANPIPQQ QAGKVEVLEF FGYPCHPAH LEPVLSKHAK SFKDDMYLRT
101 EHVVQKQKML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QRIKLQNPEV
151 LKKKLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFG IDGTEPTVVG
201 GKYKVEFADT ESGMNTIDLL ADRVREEQKA AQ*
```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

m687/q687 97.0% identity in 234 aa overlap

		10	20	30	40	50	
m687.pep		MKSRLHALL--GVAALFALAACDSKVQTSVPADSAAPAASAAAAPAGLVEGQNYTVLANP					IPI
g687		MKSRLHALLALGVAALFALAACDSKVQTSVPADSAAPAASAAAAPAGLVEGQNYTVLANP					IPI
		10	20	30	40	50	60
	60	70	80	90	100	110	
m687.pep	QQQAGKQVEVLEFFGYFCPHCAHLEPVLVSKHAKSFKDDMYLRTEHVVVQKEMLTARLAAA						
g687	QQQAGKQVEVLEFFGYFCPHCARLEPVLVSKHAKSFKDDMYLRTEHVVVQKEMPLARLAAA						
	70	80	90	100	110	120	
	120	130	140	150	160	170	
m687.pep	VDMAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQAR						
g687	VDMAAAESKDVANSHIFDAMVNQIKLQEPVLKKWLGEQTAFDGKKVLAAYESPESQAR						
	130	140	150	160	170	180	
	180	190	200	210	220	230	
m687.pep	ADKMQLTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX						
g687	AGKMQLTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX						
	190	200	210	220	230		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

a687.seq

1	ATGAAATCCA	AACACCTCGC	CCTCGGCGTT	GCCGCCCTGT	TCGCACTTGC
51	CGCGTGGCAG	AGCAAAGTCC	AAACCAGCGT	CCCCGCCGAC	AGCGCGCCTG
101	CCGCTTCGGC	AGCCGCCCGC	CCGGCAGGGC	TGGTCGAAGG	GCAAAACTAT
151	ACTGTCCTTG	CCAACCCGAT	TCGCCAACAG	CAGGCAGGCA	AAGTCGAAGT
201	CCTTGAGATT	TTTGGCTTAT	TCTGTCCGCA	CTGCGCCCAAC	CTGCAAACTG
251	TTTTAAGCAA	ACACGCCAAG	TCTTTTAAAG	ACGATATGTA	CCTGCGTACC
301	GAAACACCTG	CTTGCGTACGA	AGAAATTGCT	ACGCTCGCAC	GCCTCGCCGC
351	CGCGTCGAT	TCTGGTGCCG	CCGACAGCAA	AGATGTGGCG	ACACGCCATA
401	TTTTCGATGC	GATGCTCAAC	CAAAAATCA	AGCTGCAAGA	GCCGGAAGTC
451	CTCAAAAAAT	GGTGGGGCGA	ACAAAACGCC	TTTACGCGCA	AAAAAGTCTC
501	TGCCCGTTAC	GAATCTCCCG	AAAGCCAGGC	GCGCGCCGAC	AAAAATGCAGG
551	AGCTGACCGA	AACCTTCCAA	ATCGACGGTA	CGCCACCGGT	TATCGTCGGC
601	GGCAATATTA	AAGTCGAATT	TGCCAGCTAG	GAGTCCGGTA	TGAAACACAT
651	CGACCTTTTG	CGCGGACAAAG	TACGCGTGGG	ACAAAAAGCC	CGGCACCTAT

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

a687.pap

1	MKS K HLALGV	AALFALAA C D	SKVQTSVPAD	SAPAA S AAAA	PAGLVEGQNY
51	TVLANPIPQQ	QAGKVEVLEF	FGYFC P CHAH	LEPVL S KHAK	SFKDDMYLRT
101	EHVVQKQ E L	TLARLAA V D	MAAAD S KDVA	NSHIFDAMVN	QKIKLQEP E V
151	LKKKVLQE T A	FDGK N VLAAY	ESPE S QAR	KMOELTET F Q	IDGTPTVIVG
201	GKYKVEFAD V	ESGMNT I DLL	ADK V REEQKA	AH*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m688.pep	VLHYP	SRF	AQK	GIS	VN	KT
g688	VLHXT	SRF	AQK	GSP	VN	KT
	10	20	30	40	50	60
m688.pep	LRPGM	TKD	QV	LL	LG	SP
g688	LRPGM	TKD	QV	LL	LG	SP
	70	80	90	100	110	120
m688.pep	ILRDA	FHT	DR	WD	YTF	NT
g688	ILRDA	FHT	DR	WD	YTF	NT
	70	80	90	100	110	120
m688.pep	DVLQ	NAA	EAL	KDR	QNT	DK
g688	DALQ	NAA	EAL	RAK	QNA	DK
	130	140				
m688.pep	QX					
g688	QX					
	130	140				

```

a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51  AACCCTCATC CTCGCCCTTT CGGCCCTTCT CGGCCCTTGC GCGTGCAGCG
101 TCGAACCGGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGACAACG TCAGCTCGCGC CGTCGCCTCC CTCGCCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGGAAGC AACGCCCTGC AAAATGCCCG CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA

```

a688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSVVERVSLF	PSYKLKIIQG
51	NELEPRAVAS	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KDRSNLTLYF	ENGVLVRTEG	NALONAEEAL	RVKONADKQ*	

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

	10	20	30	40	50	60
m688.pep	VLHYP	SRAQKGISVN	KTILIALSALLGLAAC	SAERVS	LFPSYK	KLKIIQGN
a688	VLHYP	SRAQKGISVN	KTILIALSALLGLAAC	SVERVS	LFPSYK	KLKIIQGN
	10	20	30	40	50	60
m688.pep	LRPGMTK	DQVLLLLG	SPILRDAFHTDR	WDYTFNTSRNGI	IKERSNLTVY	FENGVLVRTEG
a688	LRPGMTK	DQVLLLLG	SPILRDAFHTDR	WDYTFNTSRNGI	IKDRSNLTVY	FENGVLVRTEG
	70	80	90	100	110	120
m688.pep	LRPGMTK	DQVLLLLG	SPILRDAFHTDR	WDYTFNTSRNGI	IKDRSNLTVY	FENGVLVRTEG
a688	LRPGMTK	DQVLLLLG	SPILRDAFHTDR	WDYTFNTSRNGI	IKDRSNLTVY	FENGVLVRTEG
	70	80	90	100	110	120
m688.pep	130		140			
	DVLQNAAEAL		KDRQNTDKPX			
	:::		:::			
a688	NALQNAAEAL		RVKQNADKQX			
	130		140			

1351 AAAGAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHVIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP
 301 HQYAWAFALN IITMFFNRV TAWRLKTGVH QSILLWGVV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689				SPPLPPMSGKLMMAVLMVLAVALMPFSIDAY		
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQSLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLLNLRVVQAFGAGMTVVI VGAMVRDYYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLLNLRVVQAFGAGMAVVI VGAMVRDYYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFRKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHQSILLWGVVQFAANLSQLAAVLFFGLPPFWLLVACVMF SVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF SVGTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360		370	380
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENKKRIL					
	390	400				

1109

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|||||
a689  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
      190      200      210      220      230      240
      250      260      270      280      290      300
m689.pep AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
a689  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVTP
      250      260      270      280      290      300
      310      320      330      340      350      360
m689.pep HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
a689  HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
      310      320      330      340      350      360
      370      380      390      400      410      420
m689.pep FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
a689  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
      370      380      390      400      410      420
      430      440      450      460
m689.pep DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
      |||||
a689  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
      430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTTGCAA
151 CCGGCGGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCGCCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GGACAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATCtgCctat
601 TTgaaccggC ACAACAacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCCGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACC AATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagac
751 ATCCATTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690 >:

```

g690.pep (partial)
1  MNKNTSSLPL WLAAILAAR SPSKEDKKE NGASAASSSA SSASSOTDLO
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQIIAHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEPEKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPF LD
251 IHFDENGKIT RIVVYEKNIY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCTTCCGCG TCATCAGCTC CTTCCTCAAC CGATTTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCGCG CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCAGCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPOT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
	MKNKTSSLLLWLTAIMLTACSPSKDDKTEVGASAASSSASSAPS---	QTDLQPTASAPD			
a690	MKNKTSSLLLWLAAMMLTACSPSKDDKTEVGASAASSTASAASSAPQ	TDLQPAASAPD			
	10	20	30	40	50
m690.pep	60	70	80	90	100
	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
	70	80	90	100	110
m690.pep	120	130	140	150	160
	QRLFPDIRPEDPDYHQKIIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHQKIIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
m690.pep	180	190	200	210	220
	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRL				
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLENQSLFRL				
	190	200	210	220	230
m690.pep	240	250	260	270	279
	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX				
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTITCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGCGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGOHNELEK IRAAFKMGAD RARLKVHSE HSRRRSVVEI ISSDVFNRRNE
 101 ARDYVESRYH SSMDFAVDEL EIQRHFFHIL TPQQQMWLS SCLK*

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *S. gonorrhoeae* <SEQ ID 2309>

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```
m692.seq
1 GTGTTGCACA CGCTTTGTCTG CTGTTCCGAA TCGATACGCC GGATTCCGGC
51 GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCATTAT TGGCTGCGCC
151 TTCATTCCAT CGCGGACGGG ATTATGATGCC CTGCAAGCGT TTGTGCGCGT
201 AGCGCTTGAA CGGCTCGGAG TTATAGGCT CGGTTACGCT TTTAAGCCA
251 TGGCTGTCTT TGTGCGCGT TTTGACGGCA GACCAGTTGA CATAGGCARA
301 GCTCGGTTCT TTGAACACGG TTTCCGGTCA CTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCCGCGCG GCTACGCGCG
```

1115

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCGCGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGGACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGCGCA
951 GGATGAGCGC GAGTGGGCGG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1  VLHTLCRCSE SIRRIERNR EARIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGF E RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFVDFVFG
151 NVRFCCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRGYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHI AEVADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGGKGFEE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692 98.8% identity in 336 aa overlap

      10      20      30      40      50      60
m692.pep VLHTLCRCSESIRRIERNRGREWRIKGQKCR LNTDTVQTASFYTTALFGCA FIPCGRGFVA
a692      VLHTLCRCSESIRRIERNRGREWRIKGQKCR LNTDTVQTASFYTTALFGCA FIPCGRGFVA
      10      20      30      40      50      60

      70      80      90     100     110     120
m692.pep LEAFVRVGFERFVGVIGLVYFKPLAVFVGGFDGRPDIGKARFLEQGFQGLHAAAYGVVA
a692      LEAFVRVGFERFVGVIGLVYFKPLAVFVGGFDGRPDIGKARFLEQGFQGLHAAAYGVVA
      70      80      90     100     110     120

      130     140     150     160     170     180
m692.pep VDDGKIHVGAATRQLRGFKLDDFVQVLGDVRFVGGQRI DAVFEFDPTQFVEHHQDAGE
a692      VDDGKIHVGAATRQLRGFKLDDFVQVFNVRFGCGQRI DAVFEFDPTQFVEHHQDAGE
      130     140     150     160     170     180

      190     200     210     220     230     240
m692.pep VGRVVGGRGYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
a692      VGRVVGGRGYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
      190     200     210     220     230     240

      250     260     270     280     290     300
m692.pep QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHI AEVADGRAEDDF FFRRAVVGGG
a692      QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHI AEVADGRAEDDF FFRRAVVGGG
      250     260     270     280     290     300

      310     320     330
m692.pep RSGCGGRAIFLTAAGGEDERECCGGKGFEEGFHIFSX
a692      RSGCGGRAIFLTAAGGEDERECCGGKGFEEGFHIFSX

```


1117

```

151  GRRDIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201  CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251  HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301  QVVHDEFVNV DVAHINRRA ELFOSTFDNT DCPHTSAEA ARIGKDDGFL
351  VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

	10	20	30	40	50
m694.pep	LVSASGTRQKRLKPVQTA	FAVLPHKHS----	TPASTFAQIGFGFALAA	QLFGQDEHNAFFR	
g694		SAFVLPKHMPALTPAST	FAQIGFGFALAAQLL	GQDEHDAFFR	
		10	20	30	40

	60	70	80	90	100	110
m694.pep	TLAFAYGFVPPSAYG	QCQYFP	HOHFGRGRACRYAD	FVFAKPCALQVACII	HHIRIDSARC	
g694	APPPAHGFMPPSAYG	QCQYFP	HOHFGRGRACRYAD	FAFAFKPRALQVGRV	VHHIRIDSARC	
	50	60	70	80	90	100

	120	130	140	150	160	170
m694.pep	RHFAQAVAVGRIGRT	DHNDVALFCQLFDG	GLPVGRRRIADIFL	VRIADIGETRVQRG	DDV	
g694	RHFAQAVAVGRIGRT	DHNDVALFROLFDG	GLPVGRRRIADVFL	VRIADIGETRVQRG	DDV	
	110	120	130	140	150	160

	180	190	200	210	220	230
m694.pep	FGFIDRERGLADIGE	FVGVSDFEFCHISDR	FDQKHFAARRKLPH	RSFDLVPLMPDHDD	FT	
g694	FGFIDRERGLADIGE	FVGVSDFEFCHISDR	FDQKHFAARRKLPH	RAFDLGVLMPDHDD	FT	
	170	180	190	200	210	220

	240	250	260	270	280	290
m694.pep	VLGIQSGDFLMHFRH	QASRIKHAETALRR	FLPHRLRYAVCRIN	QCRARRHFRQVFNKH	R	
g694	VLGIQSGDFLMHFRH	QASRIKYPETALRR	FLHRLRYAVCRIN	QCRARRHFRQVFDKH	R	
	230	240	250	260	270	280

	300	310	320	330	340	350
m694.pep	TFFTQVVHDEFVNV	DVAHINRRAELFOST	FDNTDCPIHTSAEA	ARIGKDDGFLVHKPG	I	
g694	AFFAQVVHDEFVNV	DVAHINRRAELFOST	FDNTDCPIHTGAEA	ARIGKDDGFSVHKFC	I	
	290	300	310	320	330	340

	360	370	380
m694.pep	SFSDGINIFLLGFY	GGRCCPTPPTPHRRRX	
g694	PCSDGIHVFLXXL	CDGRYCQAPPTPHRRRX	
	350	360	370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

a694.seq

```

1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTT CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTC TGCCAACCTT TTGACGCGCG TTTGCCGGTT
451 GGTCTGTCGA TAGCAGATAT CTTCTTGTG CGAATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 TGTGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGATGCG GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCGG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCACTCT
351 GCAAGACCGT TTGGACTATC TGAAGGCCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAAATGAA
501 AGAGCATTAC CTCATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CGGAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGCAAAACG CGCCGCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1   LPQTRPARRH HRHROYFVER KGDARSGF*C AAQCONSQRQ QSKPAL TYNJ
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVPEGSRTM
101 PTOENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYONG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQRDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCTG CTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAACA
451 CATTCTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTGA
501 AGAGCATTAC CTCATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCC
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCTGTTGAAA GGCAGGACG GAGGCGACGG
651 CGGAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGCAAAACG CGCCGCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1   LPQTRPSRRH HRHROYFAER KGDARSGFRC AAQRHPORF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQRDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHHRHROYFAERKGDARSGFRCAAQRRHPORFQSKPAERPAHRPHHPARRRR
a695      LPQACPARRHCHROQYFVERKGDARSGFRCAAQRRHPORFXSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90     100     110
m695.pep  LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT--EMSTFENASDGIPYPVPTL
a695      FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRNIQDMRLEPOAEAGSSDAIPYPVPTL
      70      80      90     100     110

     120     130     140     150     160     170
m695.pep  QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGS
a695      QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGS
     120     130     140     150     160     170

     180     190     200     210     220     230
m695.pep  ASAHTVETAQONLYNQALKHYKSGKFSAASLLKGADGGDGGIAQRSMYLLQSRARMGN
a695      ASAHTVETAQONLYNQALKHYKSGRFSAAASLLKGADGGDGGIAQRSMYLLQSRARMGN
     180     190     200     210     220     230

     240     250     260     270     280     290
m695.pep  CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPAAGR
a695      CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRS LIQTYPGSPAAGR
     240     250     260     270     280     290

     300
m695.pep  AAAAVRKRX
a695      AAAAVRKRX
     300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTCTCTCG ACGGCAGAAG CGGCAGACTC GCGGCGAGAA
251 GCCGCAGTGT CTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1  LGCRQAASHH FCQGNKLFVG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1123

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCG
 151 CGCGTGGAGG ATTGGGTTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
 301 GTCGCGGTGT CGGGCAGTGT CGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCGGC AAAGTATGTC GCATATTTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
 451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCC
 501 GTTGTCGGTC TGGTTTATGC TTTTATCTCT TCGGGCGGG CTGCTGTTT
 551 CCGCATCGAC AGACGGGTGT TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGTT GGTATTCCTT CTGGGTTTGT GTCATGACCG AGGCTTACGG
 651 CGCGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG
 751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGGTGCGGGC GGTGTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTC CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKKGVS
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPES ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVFSA
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVVKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVVKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQGCVLLGFAFG					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVRQGCVLLGFAFG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIALNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIVIRAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
	I					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGCC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTGCATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAACTTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGCT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCTGTC GCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG
51  FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGCC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTGCATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPHAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC SGTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPEAGLMVWVAPNSFAS	FKRFSISQT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVWVAPNSFAG	FKRFSISHT			

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVFPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLM K TAPASSTALS
51  CSGLVTVFPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

```

m702/g702
      10      20      30      40      50      60
m702.pep  MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVFPAP
          |||||  |||||  |||||  |||||  |||||  |||||
g702       MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCKPGLMAKTAPASSTALSCSGLVTVFPAP
          10      20      30      40      50      60

      70      80      90     100     110     120
m702.pep  TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS
          |||  |||||  |||||  |||||  |||||  |||||
g702       MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS
          70      80      90     100     110     120

      130     140
m702.pep  RGVSLDISVL RVEWGILLRW DRLX
          |||
g702       RGVSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVFPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTPAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

```

      10      20      30      40      50      60

```

1129

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

```

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGVVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSEDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGVVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSEDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPSEDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAACGCTT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1131

```

801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCCCT GCGTTTTTGC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTGCGCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGGCAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAI
1301 TCGGCGAACT CCTGCTTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTGCG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCCTCG CCCAAACCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCGG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGCG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCGCTCAA GACAGCGCGG CGGAGGCGGT CCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGACGCGC CCTGGGTGT CGCGACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATGTGTGTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGG AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCACTCTGA
2451 AAAAAAGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

a704.pep

```

1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLE QLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLMMQTM MFALPTYLYG
201 GDIEPDFLQI LHWGGFLMVL PVVFCAPVF YQALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGO GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEAEQYAS SFIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSSGFGQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHL SGRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLWAG AYNIIAVPLA VLGYPQFWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFFVETHGGTREAVLMLGGITCAACVWLEEQLLRTDGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFFVETHGGTREAVLMLGGITCAACVWLEEQLLRTDGIV

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```
g705.seq
1   GTGTTCAATA ATTCCTttgc CTCTCTGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGTCCTTgcC TTTGGCGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTCCAAAA
201 ATGCTTGTGT AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC GTCCGTCGCG
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GCGGATTTTG TCCGTGCCGA
401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTTCAAAA CACCTCGCTT GCCGCCGTGG
551 TAACCGTAAC GGAGCTTTTC CGTGTGCAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGTTT
651 CTGTAAAGTG CTGTTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GTTATGTCCG CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```
g705.pep
1   VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFOKCLL KLVEFYISVV RGTPLLVLV IVFYGLPSVG
101 IYINPIPAAI IGFSLVNGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRIYVAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```
m705.seq
1   GTGTTCAATA ATTCCTTTCG TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGGCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTTG CTTTGGTTCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCCGTCGCG
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TTGTGCGGCC GCAGGCATTC CGCGTTGCCG TGCCGCCCTT
501 GAGCAACGAG TTTATCGGTT TGTTCAAAA CACCTCGCTC GCGGCAGTCG
551 TGACCGTAAC GGAATTATC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTTCTCGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```
m705.pep
1   VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSLVNGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRIYVAK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```
m705/g705    95.0% identity in 238 aa overlap

              10      20      30      40      50      60
m705.pep     VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g705          VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
              10      20      30      40      50      60

              70      80      90     100     110     120
m705.pep     AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIIYIDPIPAIIGFSLVNGAY
              :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

```
g706.seq
1  ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgcccGCTGGC TCAACTCCTA
51  CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cggtgGAacg taTGctcggg acggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTATGGC TGAACCAGCA TTAttttccac
301 ggcaaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctga
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCTAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

```
g706.pep
1  MNSSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFAFA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RMTREERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE ROHLRQSLLE TREHG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

```
m706.seq
1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC CGCGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCAAGCT
801 GCAATCTCCC AAACCTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

```
m706.pep
1  MNTSQNRNLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYKAVVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RMTREERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
```

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACAGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWFDSD
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSRLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
m706	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPMLAGLTMCMLIGDNGSEWFDSDGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPMLAGLTMCMLIGDNGSEWLDGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSRLAATSGESRISP					
m706	FMLADNLADCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSRLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
m706	AMMEAMQHAHRKIIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLLETREHSX					
m706	RQHLRQSLLETREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGGCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTC CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTC CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTGCGCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEEKRD KSAEGSISAF NNXKPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIPIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERM
251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHRLAYL
301 RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90      100

              40      50      60      70      80      90
a707.pep    GYLTSQAIQPQNMDSGILKLRVSAGEIGDIRYEEKRDKSAEGSISAFNNKXPLYRNKI
              |||
m707      GYLTSQAIQPQNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNKI
              110     120     130     140     150     160

              100     110     120     130     140     150
a707.pep    LNLRDVEQGLENLRLPSVKTDIPIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              |||
m707      LNLRDVEQGLENLRLPSVKTDIPIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170     180     190     200     210     220

              160     170     180     190     200     210
a707.pep    GK YQGNVALS XDNPLGLSD XFYVSYGRGL VHKTDLTXATGTETESGSRSYSVHYSVXVKK
              |||
m707      GK YQGNVALS FDNPLGLSD LFXVSYGRGLAHTD LDTATGTETESGSRSYSVHYSVPVKK
              230     240     250     260     270     280

              220     230     240     250     260     270
a707.pep    WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXFXXTSVXMKLWTRQTY
              |||
m707      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKT SVGMKLWTRQTY
              290     300     310     320     330     340

              280     290     300     310     320     330
a707.pep    KYIDDAEIEVQRRRSAGWEAELRHRLAYLXRWQLDGKLSYKRGTGMRQSM PAPEENGSGT I
              |||
m707      KYIDDAEIEVQRRRSAGWEAELRHRLAYLNRWQLDGKLSYKRGTGMRQSM PAPEENGSGD I L
              350     360     370     380     390     400

```

1141

```

      1 MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
     51 DYRQATASIE DALKSDPKNE LAWLVR...Y QYLVNDKAQ ESFRQALSIK
    101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
    151 SAKQGQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
    201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
    251 TGQ*

m708/g708 99.2% identity in 253 aa overlap

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRLNR
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRLNR
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFAFKE
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPFAFKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
      1 ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
     51 GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
    101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
    151 GACTACCGTC AGNGACGGC AGTATTGAA GACGCCTGA AATCAGACCC
    201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
    251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
    301 CCCGACAGTG CCGAAATCAA CAACACTAC NGCTGGTTCC TGTGCGGCAG
    351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
    401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
    451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
    501 CCTCGCCGCC CAGCCGCACT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
    551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
    601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
    651 GAAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
    701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
    751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
      1 MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
     51 DYRQXTASIE DALKSDPKNE LAWLVR...Y QYLVNDKAQ ESFRQXLSIK
    101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
    151 SAKQGQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
    201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
    251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCAATTGG
 101 AGTGGTTGCC GCATATGTCC ATTTATGCCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGCATGAT
 201 AGGCGCGTTG AATCAGGGA TGGCGCGCAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCTCCTT
 351 CCGCTGTGT TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGCGG GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGCGG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG
 651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
 701 CCGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCCTT GTTGGTCATT
 751 TTGGCATTGA TGCGCATCAA CGCCGTCGTC GCCATGCTCT TACCGTCAT
 801 GGTTCGCGTT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTT GCGCGCGCGT TTGGAAGTA TGTTTTTCAC
 951 CGAAACCATC GTGATTCTCG GGATGATTTT GGGCGGACTG TTGTTTGCCT
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
 1051 GCCCGACGCG CGACGTTTCA CGTTGCCATG ACTTCGTCG GGGTTAATTT
 1101 CCGTATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTC
 1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
 1251 CGCGGTGTTT ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTCGGT
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDMPRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYFGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFOA
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTTIP
 201 AMLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAIRFTLTN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDMPRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDMPRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQGMIGALNQMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQGMIGALNQMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVA FMGMAAFOADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTTCATVGVA FMGMAAFOADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFEHIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFEHIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLPHMSIIAAIVVLILYGLARGLKYN				
m709	MFAFKSLDMPRGEALAVVVALIAAMGYTII	SLEWLPHMSIIAAIVVLILYGLARGLKYN				
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIP	TLMYYGFLISPTYFYFS	AFALC		
m709	DMQQGMIGALNQGMGAIYLF	FFIGLMVSALMMSGAIP	TLMYYGFLISPTYFYFS	SSFALC		
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGVA	MXXXXAFXAXMXXXXXIVXXAXXGKMSPLSDTXG	XS			
m709	SVIGVSIGSSLTTCATVGVA	FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTG	ISA			
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMMYTTIP	AWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLV	HCY			
m709	SIVGIDLFEHIKNMMYTTIP	AWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLV	HGY			
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNAV	VAMLF	TIVAAVAVTYLHSTPDLRQLGAWFYGGYKLEGE	AXX		
m709	SLIPFALLVILALMRINAV	VAMLF	VMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGE	AFK		
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLES	MFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLT	NAGRXTFSVAM			
m709	DVVKLISRGGLES	MFFTQTIVILGMSLGGLLFALGVIPSLLEAIRFTLN	AGRATFSVAM			
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEYQYLSI	LLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF			
m709	TSVGVNFLIGEYQYLSI	LLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF			
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYAFFCY	LSLALTLLFGWTGLTLSKKX				
m709	ISHALGVPVWEYLPYAFFCY	LSLALTLLFGWTGLTLSKKX				
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCGCGGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1   ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGAAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCC CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
851 TTGAAAAACA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1   MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1   ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGAAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCC CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```


1149

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAAACA CCCCCTTTG GCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCACTGGC GGCTGGAGGG ATTTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGCGTGA GCCATAAGGG
1101 CAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1  MQNNSYGYAV SVRVGKKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMIDIEWDTD NRFSEVFLA QSHGRSGDSA KHDLEWVYKD PTMTLHRPKT
251 VVVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGLR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGK GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAAACA CCCCCTTTG GCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCTG
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGCGTGA GCCATAAGGG

```

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CCGTACGGGC AAAAACCGCC AGCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```

m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CCGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A

```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```

a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPRSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNVRG GNNRITRFRAGISAAGDRLT DYSDAVIESL FNRLKPAHTA					

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVPAHKPASNATGVOKSAQGSAGSCGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
g716	SCGAASKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMOTAAGLTV
 51 SVLCLGLDOA YVREYYATAD KOTLFKTLFL PPLLSAAAIA ALLLSRPSLP
 101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
 151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
 201 HAPFSPAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
 251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
 301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
 351 RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
 401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAYLAG
 451 CILHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
m717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMOTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMOTAAGLTVSVLCLGLDQA					
m717.pep	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
m717.pep	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
m717.pep	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
m717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTSVLTAVYALA					
m717.pep	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
m717.pep	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCRLKAVRRAPFSPAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY					
m717.pep	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
m717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
m717.pep	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
m717.pep	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT					
m717.pep	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
m717.pep	LGALAANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALAANLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
m717.pep	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
m717.pep	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
g717	CLASSAAYTCFGTPANYPLFAGVWAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
m717.pep	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
 51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
 101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGCGCGG GCTGACGGTG
 151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCTG CCGCCGCTGC

```

|||||
m717      AGLEQLGVYSMGISFGGAALLFQSI FSTVWTPYIFRAIEENAPPARLSATAESAAALLS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||
m717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAANLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||
m717      LGALAANLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLHFHYLKKQGFP LX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCI: LHRKDLHKLHFHYLKKQGFP LX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1      TCAGACGGCC TTTACGTACC CCGAACTTT ATCCACCGCC CGCAAAGCTG
51     GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101    CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151    TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201    GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTGCC GAGTTTGTGG
251    AGCTGTACGG CATGCCATC CGTATCGCA AATACGGCG GGGCGCAACC
301    AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351    CGCGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401    CAAACGGTAC GACGGCAACC AGCAATCCGT TTTGCAGAT GGCCGACTGG
451    TGCGAAAAAT CGGCGCGCGG GCTGATTTC GGGCAAACGC TGACGACGGG
501    TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551    TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601    ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651    CCCAAACCGC GTGCCGAAAT TTGAATTGA CACGCGCGAG CCGAAAGACA
701    TCGCGTCTT TGCCGACGCT ATCCGAAAC TGCTGGATGT CGGCGTACAA
751    ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCAATCCAG ATGTGCAGGA
801    GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAACAGAA
851    CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901    AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951    CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001   TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051   TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101   GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1      SDGLYVPRNF IHRPQSWFKW DKDNGLLLR RENPEGEALW PLGWVHTQK
51     SRSVQQARNG LFRTLRWLYM FKHYAVHDF EFLGYMPI RIGKYGAGAT
101    KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTAT SNPFQMADW
151    CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRDLLV SDAKQVAQTI
201    TSQIIGPFLQ INYPHADPNR VPKFEFDRE PKDIAVFADA IPKLVDVGQ
251    IPESWVRDKL VIPDVQEGEA VLVROVPDNP VNRTALAALS AHTVPSKATG
301    RHQEILDGAL DDALVEPDFN SQLNPMVROA VAAALNACNSY EEADAALNAL
351    YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVVDVGVIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVVDVGVIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHRAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHRAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCCTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGCG GCGTGGTGGC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGCGAG GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAACTTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGCACG CTTTCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGCGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 CGCGCGCGCG TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCAAC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTG GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCT GCGTACAAAT CCCGAAAGC
1201 TGGGTGCGCG ACAAACGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGTGTCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTG
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACCGCA AACTGCGTCA CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPOKMRA
51  LFEDAESGDI RAQHELFADI EERDSIAAN MGTRKRALLT LNWVRVAPPRN
101 ATPEEELSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQMAADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

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1163

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLWSLYMFKHYAVHDFAEFLGYGMPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLWSLYMFKHYAVHDFAEFLGYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKOVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKOVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRPVKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRPVKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGGCGC	GCAGCGGCAA	GGCATCACA	AATGATTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTGCGGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCGGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTGCG	CGGTTTGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCTCTG	CGAAGCGGCG	ACTAATGTGC	AAAACTTTT
951	GAGTAAACT	CTGTCGCCTG	ACACGATAGG	TCGCTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGATG	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGACG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGCGC	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTGTGAG	GCAAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TCCAGACGSC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGCGG CAGGCCGTCT GAATGCGTTG GTTGGCGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHAKPFVQ GIDLEDMGMT
51 GRQVQINAVF WKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGCGGGTC ATCAACCAAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNRLNRLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESELRAAA
101 GRLNALVAAV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HIHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

                250      260      270      280      290      300
m720.pep      SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQPVQAQAVRLLSTSSLL
                |||||||||||||||||||||||||||||||||||||||
a720          GLQNRLNRLTAKQVQPVQAQAVRLLSTSSLL
                10      20      30

                310      320      330      340      350      360
m720.pep      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                |||||||||||||||||||||||||||||||||||||||
a720          SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                40      50      60      70      80      90

                370      380      390      400      410      420
m720.pep      QTAESELRAAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
                |||||||||||||||||||||||||||||||||||||||
a720          QTAESELRAAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
                100      110      120      130      140      150

                430      440
m720.pep      HIHHPAFIKRGTLVNSYAKX

```

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51  NGHDVALLAN SSRNQLVVYD EH*TLYKEKN GQPAPAAGWM RWLEFTPCKGM
101  FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGVVSKIFHA ALTNFFALDG
151  MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201  KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251  AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301  ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351  EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVP	10	20	30	40	50	60
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVP	10	20	30	40	50	60
a721.pep	SSRNQLVVYDEHXTLYKEKNGQPAPAGWMRWLEFTPCKGMFAEVEWTDKAAAAIAAKEYR	70	80	90	100	110	120
m721	SSRNQLVVYDEHQTLYKEKNGQPAPAGWMRWLEFTPCKGMFAEVEWTDKAAAAIAAKEYR	70	80	90	100	110	120
a721.pep	YISAVFSYDTKGVVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF	130	140	150	160	170	180
m721	YISAVFSYDTKGVVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF	130	140	150	160	170	180
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI	190	200	210	220	230	240
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI	190	200	210	220	230	240
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI	250	260	270	280	290	300
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI	250	260	270	280	290	300
a721.pep	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX	310	320	330	340	350	
m721	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101  ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151  CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201  TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GAGCCGCCGC AATCCTACCA
251  CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301  GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351  CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCAGGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTGCGGAT TTCGTGCGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTG GCAGTGGCGT
351 CCACCAGCGC GGTTTGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTGCGGCCA GCCGCGGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTGAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTCTGCGT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAALIIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LUVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRONSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSAESAFLLS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAUVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pet not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCAGCTTTTTCGCCGTGTTTACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTGTCGTCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+ 120
GACGCGCGCGGAAAGCCCCTTTTGTAGTGCAGACCACACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCGACGCGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGGCAAT
601  ATATCGTTGC  GCCAGCACCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

a724.pep

```

1  MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKLNK
101 PGETAIFNHE  GAKIVIKQ GK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNAFL
151 VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201 ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPGETAIFNHEGAKIVIKQ GK					
m724	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPGETAIFNHEGAKIVIKQ GK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFN TDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFN TDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

m725.seq

```

1  ATGGTGCGCA  CGGTTAAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
51  GCAAATCCAT  ACGCTGCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101 TTGAGCCTGC  CAGCACCGGC  GGC GTATGCG  GACGTATATCA  GGATACCGCC
151 GAATTTGTGG  TGATGGTGGC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201 GCGGCAAGGC  GGCATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251 GCGCTGTTTC  CCGCCTGCTT  GACGGCCAGC  GGCTCGGTTT  TGCCGATAGC
301 CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGGT
351 GCAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401 ACACCTGCGG  GTTGAAAAAT  GACCGCTACC  CCGAACGCAC  CGACAATCCC
451 GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501 GTGGCCTGAT  TTCGAGGGGT  TGGACGCGAA  AATTACGAC  CCGCAATCCG
551 CCGATGAAAT  ACCTGTAAAC  CTAACCCTTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

m725.pep

```

1  MVRTVKSUNG  EADDLAQIHL  TPAVWVTYGG  GSKVEPASTG  GVCGRYQDTA
51  EFVVMVAARN  LRNEQAQRQG  GIDSREIGSN  DLIRAVRRL  DGQRLGFADS
101 RGLVPKAVRA  IANHVVLQNA  AVSIYAVEYA  IRFNTCGLEN  DRYPERTDNF
151 DDPNHIFTKY  QGTLSEPWPD  FEGLDGKIYD  PQSADEIPVN  LTLKDKQ*

```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:::|||||:||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAQKQTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKLNIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51  AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPFD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51  CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAA
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTGTCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51  AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMKRDKAQALLLSAQN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1175

```

501  CGGGGAAAAT  TATGAAACGA  CAGGAGAATA  TCGGGTTGTT  TGGCAACCAG
551  ACGGTTTCGGT  ATTGATGCG  GCGGGGCGCG  GGAAATCGG  GGAAGATGTT
601  TATGAGCATT  GCCTCGGGTG  TTATCAGATG  GCCCAGGTAT  ATTTGGCGAA
651  ATACCGGGAT  GTCGCGAATG  ACGAGCAGAA  GGTTTGGGAC  TTCCGCAAAG
701  AGAGCAACCG  AATTGCGTCG  GACTCGCGCA  ATTCTGTGTT  TTATCAGAAT
751  ATGCGGGAAT  TGATGCCCCG  AGGGATGAAG  GCGAACAGTC  TTGTGGTCCG
801  CTATGATGCG  GACGGTCTGC  CGCAAAAAGT  CTATTGGAGT  TTCGACAATG
851  GAAAAAACG  CCAGAGTTTC  GAATATTATT  TGAAAAACGG  AAATCTTTTT
901  ATTGCACAA  CTTCGACGGT  AGCATTGAAA  GCGGATGGCG  TAACGGCGGA
951  TATGCAGACC  TATCATGCGC  AACAGACGTG  GTATTGGAT  GCGGGCGGGA
1001 TTGTCCGCGA  AGAGAAACAG  GGAGACAGAC  TGCCTGATT  TCCTTTGAAC
1051 TTGGAATAAT  TGGAAAAAGA  GGTGCGCCGT  TATGCAGAGG  CTGCGGCGAG
1101 ACCTTCGGGC  GGCAGGCGCG  ACCTTCTCA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSV DA AGRGKIGEDV
201 YEHLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGYYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVVPENPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m728.pep	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1177

	180	190	200	210	220	230
a 728 . pep	WQPDGSVFDASGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDASGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFRKNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a 728 . pep	DSRDSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a 728 . pep	IAQSSTVALKADGVTDQMITYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEKEVSR					
m728	IAQSSTVALKADGVTDQMITYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a 728 . pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729 . seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTGGGGTT GGCATGACTA TTTTCCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGCGGg
351 caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCGa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCG GCCGTGCCCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GCGCGCAAT GCCTTGCGAA CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGg TTTGCCGTG GACAagcAGT TTTTGTGTA
801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCGg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTAATTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGATTTGC TCGATGCGGA ACGCATCAGC TATTCGCGCG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729 . pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```

1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERN	TSRLTAVLNSEI	YRKQYMIERN	NLLPTLAANAND	SRQGSLSGGNVS	
g729	PRLQKLIDIALERN	TSRLTAVLNSEI	YRKQYMIERN	NLLPTLAANANG	SRQGSLSGGNVS	
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGLGAASYEL	DLFGRVRSSEAA	LQGYFASTANRD	AAHLSLIATVAK	AYFNERYAE	
g729	SSYNVGLGAASYEL	DLFGRVRSNSEA	LQGYFASVANRD	AAHLILITVAK	AYFNERYAE	
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTR	EETYKLSELR	KAGVISAVALRQ	QEALIESAKAD	YAHAARSREQ	ARN
g729	KAMSLAQRVLKTR	EETYKLSELR	KAGVISAVALRQ	QEALIESAKAD	YAHAARSREQ	ARN
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPED	LPAGLPLDKQF	FVEKLPAGLS	SEVLLDRPD	IRAAEHALKQ	ANANIGA
g729	ALATLINRPIPED	LPAGLPLDKQF	FVEKLPAGLS	SEVLLDRPD	IRAAEHALKQ	ANANIGA
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTG	TGVTGSAELG	GLFKSGTGV	WSFAPSITL	PIFTWGTN	KANLDVAKLRQ
g729	ARAAFFPSIRLTG	SVGTGSVELG	GLFKSGTGV	WAFAPSITL	PIFTWGTN	KANLDVAKLRQ
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQ	SADFQVANALA	AREQLDKAYD	ALSKQSRASKE	ALRLVGLRYK	HGVSGA
g729	QAQIVAYESAVQ	SADFQVANALA	AREQLDKAYD	ALSKQSRASKE	ALRLVGLRYK	HGVSGA
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYA	EGAALSAQLTR	AEENLADLYK	ALGGGLKRD	TQTDKX	
g729	LDLLDAERISYA	EGAALSAQLTR	AEENLADLYK	ALDGGGLKRD	TQTDGKX	
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATG GATACTA CATTGAAAAC CACCTTGACT TCTGTGTCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGCGGCA ACGTGTTTTG AAAACGCGCG AGGAACCTA CAAGCTGTCT
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCGAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCCG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTTCCT ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGGTGTGGT
1001 TGTTTCGACC TTCCATTACC CTGCCGATT TTACTGGGG TACGAACAAG

```


1181

```

          430      440      450      460
a729.pep  LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          |||||:|||||
m729      LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

```

g730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGTCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGCAGC  GTTTCGACCC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCACCCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGGTT  ACACCGTCCG  CTTTTCGGGA
301 CACGGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCGAAG
451 GCGCGCAATT  ACCCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCGCGA  GTATCAAACG  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGCGCAACAT
801 CGCCCCCTTA  CCCGCGGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGCGGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAAACCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCCTTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCCCTG  TTTCCAACCG
1251 CATCCACCCG  TTTTATTCGG  ACGGCAAATG  GATTAAGGCG  GAAGATTTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAACCCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTTCGG  AAGGAAAGCA  ATATTTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```

g730.pep
1  VKPLRLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQAAAIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEHGEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTAGDY  KAIAHIQAGD  RVLSKDEASG  ETGYPVTAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYSDGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  PPKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYV  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

```

m730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCGCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAALPGKAAVSGDFSKSYTCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAALAKAALPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GGCGGCGGCA  CTCATACAGC  CCGCCCTCGC  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACCCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCCCG  ATGCCCTACG  CGGCCCGAAG
451 GGCGGCAATT  ACCCAAACCC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACTAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACTG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAT  ATAACCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRLRIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEHGEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARIKLNPT  DTSIRQRIS  DNYSNLGSNF
201 SDRADANRK  MFEHNAKLDR  WGNSEFING  VAAGALNPF  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAKAAL  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

```

1185

```

251  GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301  CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
351  TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

```

m731.pep
  1  MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51  NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
101  HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

g731/m731 95.2% identity in 84 aa overlap

```

                                10      20      30
g731.pep                      DFRAFSCENGLSVRVRNLDGGKIALRLDGR
                                |||||
m731      LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHLDGKVALRLDGR
              20      30      40      50      60      70

              40      50      60      70      80
g731.pep    RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
              |||||
m731      RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```

a731.seq
  1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
 51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
101  CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCCAG
151  AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
201  GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
251  GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301  CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
351  TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

```

a731.pep
  1  MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51  NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
101  HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

a731/m731 94.4% identity in 126 aa overlap

```

              10      20      30      40      50      60
a731.pep    MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCEGLSVHVRRL
              |||||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHL
              10      20      30      40      50      60

              70      80      90      100     110     120
a731.pep    DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
              |:::|||||
m731      DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
              70      80      90      100     110     120

a731.pep    TSCRARX
              |||||
m731      TSCRARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

```

g732.seq
  1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51  CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
101  ACGGgcgGGA TAACGAagtC CTGCCGTGC AATCCATCCG TACGATGGCG

```

1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGCGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMEK KGYAEIKEST
101 SGEGGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAIL KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKKD KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGF	AAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY				
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGF	AAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEGGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEGGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRITMAEVYGGQIKANY					
m732	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRITMAEVYGGQIKANY					
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKKGKPLKGLV					
m732	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKKGKPLKGLV					
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
a732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKGSVQTLIPLSNGSAV					
m732	310	320	330	340	350	360
	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKGSVQTLIPLSNGSAV					
a732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRSIAAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	370	380	390	400	410	420
	KLTTALYYTPNDRSIAAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
m732	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
a732.pep	490					
	PVSNKDKKDKKKX					
m732	490					
	PVSNKDKKDKKKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGIGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCATTTCG GACTGCTGTC

```

1191

```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLNDDTS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              |||
m733          MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERLFPESGVFMDFLMKTGKG
              |||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              |||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYQ AQGQCGLETV YCTSSSYYG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCCG TCGTGTGCGT
51  GAACAATACC TGTGTGCGCG TGGCATACCC GAAAGCCTTG GCGCGCTGCG
101 GTGTGACAAA CGCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGCGGTAC AGGGACAATG
201 CGGCTTGGA ACAGTGATT GCACATCTTC TTCTATTAC GCGGGAAGT
251 TCGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAV VITSPRFTSVH
51  QVALNQCIKK YGVQCGGLE TVYCTSSSY GGTVRSIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGCTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
a735.pep	YARELEQARAEAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTTGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCT TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTCG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTCG AACGTCGCGG GCATTTTTCG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCIP*SEGILRASTRVTVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTC	CGT	CGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA	
101	CGGCTTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTGCCCGGC	
151	GTGCTGTCCG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCCGCATGGT	
201	CTTGGGTTC	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA	
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG	
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA	
351	AATCGGTI P3	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG	
401	CGGTAACCC	CGTCGCCCGA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG	
451	TTTTCCATGC	CGCTTTTGGC	TTCGATTTTC	AACGTGGCGG	GTATTTTCGG	
501	CGCGTATTTG	GTCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT	
551	GGTCGCAAT	GCAGAACAA	ATCACGATAC	AATACGATGT	AATCAACGGT	
601	CTGATCAAAT	CCGCCCGGTT	CGGCGTGGCG	GTAACGCTGA	TTGCCGTGCA	
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA	
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	CGATTTTATA	
751	TTGACCGCGT	GGATGTTTAC	AGATTGA			

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMAVNPVAR	VVAPRFWAGV
151	FSPMLLASIF	NVAGIFGAYL	VGVTWGLGDS	GIFWSQMNN	ITIHYDVING
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRVTVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWGLGDS					
m736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWGLGDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS					

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a737.seq
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
 1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
 51 AQA EKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQA EKAALAR
m737	MNIKHL	LLTSAATALLS	ISAPALAHHDGHG	DDDHGHAHQ	HNKQDKIISR	AQA EKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDLE	HDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
 1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCG CCAAACCTGCC
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
 151 GCGGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTCG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAAACA TCATCGTTCA
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCCTCG CTTACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAAGC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
 951 CGGCTGGAAC AGTTTGGCC AACAAACCTT CTTGATCAAT GCCGAACAGC
 1001 ACACCATAA CGACAACTTC CTCAGCACCT TGTTCAACCA TTCCCACAAC
 1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
 1151 CCCCCGCATC ACTTTTCTCG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCTCG
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
 1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
 1401 CCCC GCCGCT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAAC
 1451 TGGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCTTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCCTAC TCCGCCACCT

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLP	IIYILPCFLWIGIVPFT	FALKLKPSPDFYHDA	AAAAAGLIVLLFL		
g738	MSAETTVSGARPAAKLP	IIYILPCFLWIGIIPFT	FALRLKPSPDFYHDA	AAAAAGLIVLLFL		
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
g738	TAGKKLFDVKIP	PAISFLLFAMAAFWYLQ	ARLMNLIYPGMNDIV	SWIFILLAVSAWACRS		
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
g738	VAHFGQERIVTLFAWS	LLIGSLLQSCIVVIOF	AGWEDTPLFQNIIVY	SGQGVI	GHIGQRN	
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
g738	NLGHYLMWGILAAAYL	NGQRKIPAA	LGVICLIMQTAVLGL	VNSRTILTYIAAIAL	ILPFW	
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
g738	YFRSDKSNRRTMLGIA	AAVFLTALFQFSMN	ITILEFTFGIRYETA	VERVANGGFTDLPRQI		
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
g738	EWNKALAAFQSAPIF	GHGWNSFAQQTFLIN	AEQHNIDNLLSNLFT	SHNIVLQLLAEMG		
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
g738	ISGTLVAATLLTGIAG	LLKRPLTPASLFLICT	LAVSMCHSMLEYPLW	YVYFLIPFGLML		
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
g738	FLSPAEEASDGI	AFKKAANLGI	LTA	SA	AFAGLLHLDWTY	TRLVNAFSPATDDSAKTLNRK
	430	440	450	460	470	480

1201

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201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTSHSN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFAPEY PETOTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQPSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPISFLLFAMAAFYWLQARLMNLIYPGMNDIVSWIFILLAVSAWACRS					
m738	TAGKKLFDVKIPISFLLFAMAAFYWLQARLMNLIYPGMNDIVSWIFILLAVSAWACRS					
	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
	VAHYQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
	YFRSDKSNRRRTILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
	EWRKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTSHSNIVLQLLAEMG					
m738	EWNKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTSHSNIVLQLLAEMG					
	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
	FLSPAASDGI AFKKAANLG ILTASAAI FAGLLHLDWYTYRMVNAFSPATDDSAKTLNRK					
m738	FLSPAASDGI AFKKAANLG ILTASAAI FAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
	INELRYISANSPMLSFYADFSLVNFAPEYPETOTWAEATLKSLKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFAPEYPETOTWAEATLKSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPQHTDSPRET					
	: : : : : :					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT					
	: : : : : : : : :					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
	:	:	:	:	:	:
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
	: : :					
g739	PKNTPAKPKHEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACAA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFER LTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLFX*

a739/m739 93.9% identity in 197 aa overlap

10 20 30 40 50 60
a739.pep MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPQHTDSPRET
|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPQHTDSPRET
10 20 30 40 50 60

70 80 90 100 110 120
a739.pep EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKQPADTAQT
70 80 90 100 110 120

130 140 150 160 170 180
a739.pep DRQPDDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD
|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739 DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
130 140 150 160 170

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1205

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a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m740      LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTCT
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCCGCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAA GCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCTG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAG CCGAGTATCA CGGCAAGCA TTCAGTCCG
551 ACGATGCGGA CGGAAACTG ACCTATACCA TAGATTTCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAEKTFK AGGKDNSLNT GKLNKDISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHSA VVALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCCTAACCG GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GGCGGCACAA GGTGCGGAAA AAACCTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTTCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTGTA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLLAAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQYKQ SHSALTAFQT EQIQDSEHSK KMAKROFRI

```

1207

q742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```
m742.seq
1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGTGCTTAC
51  TTTGGGCGCG ATGTATCAGA AGACTAGGGA GGTTCTCTGAT TTTTCGGGCA
101 TTAATTTCGCC CTGTGAAAT CAGAAAACTG CCCCGTTCAG TTCACAGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAATACAA CCTTTCTCA TGGAATCAAA
251 ATGTGTTTCA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGCGAGTTT TTTCTGAAA ACGAATATGC
351 GGCGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGACT GAAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACGCCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGTTTTCGA ACGATTCTCG ACCCGCGTGT
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCGTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGCGGGAA TTTGTCGATA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCT AACAGCTGTG ATGACTCTTC CTTTAACTCG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTTCGGCG GGAGCATGAT TTCTTTGTGC GCTATGCCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACCCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACCGGCTGTA TGCGGAAGT GTGCAGGAGT
1001 AGCCGGACGG CGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATCAGGAAGC GCCAAGAAAA TAAAACCGCA GCCCAAGCTC GATGCCGGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA CGGGCAGCCG GACACGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCAGC GGCACGCGCT CTTTACCCTG TTTTCCGGT ACGGTGCCCG
1301 TTTGGAAAAA CGTCAAAGTG CGACAGCACC ATGTTCTCTG GCTGTATAAC
1351 TAGGCCAAAT ACCTCAACAC CAACAAAACC CATTCTGCTGA CTGCCAGTAC
1401 GCGTTTCAAC GTAACCGGCC CAGTCACCTT TTTGGCGGGG CTCGACTACA
```

1209

```

1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATAT AGGTAGGCTG GAAAGCGCGG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCTGCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGTGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCTCGCC AAAACACAG GCGCAGACC GTACAACTT AGCAATTTCA
2051 CACCCGTGCA CATATTCCTT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGCGGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACCTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N Q K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E H A A G L S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D E C M S A P F A
201 L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D P Q W C T Y L D L T G T Y G L F G R E H D F F V G Y A Y S T E
301 K I R S E Y L E I Y E R R H R V R P N T G A T H G V Y A G S C Q G E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A G T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I K A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N T G A D P Y N F S N E T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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a742/m742 98.5% identity in 783 aa overlap

```

          10      20      30      40      50      60
a742.pep  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N Q K T A P F S S T P A C N R P L Q L P R
          |||||||
m742      M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N Q K T A P F S S T P A C N R P L Q L P R
          10      20      30      40      50      60

          70      80      90      100     110     120
a742.pep  N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E H A A G L
          |||||||
m742      N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E Y A A G L
          70      80      90      100     110     120

          130     140     150     160     170     180
a742.pep  S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
          | |||||||
m742      S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
          130     140     150     160     170     180

          190     200     210     220     230     240
a742.pep  S R R A A E R K A G F D E C M S A P F A L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P

```

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ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)
 pseudobactin uptake protein (*Pseudomonas putida*) Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPKQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGVYPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + +G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEGLVPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRWNTYRLPGWEKLTGGGVNWNNSKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY---YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTATATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAG
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTGTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGCGG GGTATTATGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSRLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPPG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTATATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGC
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAG

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGA AAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAC TGA AACTGAA TATTTAATA TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
1 MKPLKLTLEFG FVDAANYRRR ENKDLFNRF VKGEYLDLCL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNON TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQEQKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLOFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPRIKTETE YLIFSGLSKA LDVGTFFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
1 ATGTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT TACTACCGTA ATCAATCGGC ACGAGTTTGA TGGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
1 MFWQLTVYSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPLV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
1 ATGTCCGAAA ACAAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACC GGCGCA ACGGAAGCC AACGGCAAA
201 CACGGCACAA ACCCTGCTCT TGAATCCGC CGCCGAAAAC GGGGAAACCG
251 CGCCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGA A ACGTA GCGCGGCCGC TGGTCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGTTTGGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACCTGCCG AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAA TGCTGCCGAA AAAACCAAC CGGATACGGC
651 AAAATCCGAC AGCCCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

a746.seq

1	ATGTCGCGAA	ACAAACAAAA	CGAAGTCCTG	AGCGGTTACG	AACAACCTCA
51	ACGGGCGCAC	CGCCGCGCCG	TCGTAACGGT	AAGTGTGCTT	GTTTGGCGCT
101	CTCGTCATCT	GCTTGGCAGC	CGCCTCAGTT	CGGGCCCTGC	GGAACAGACT
151	GCCGCGCGAA	CAAGCGCGCT	AGAAAACAAA	GCGGCAGGTG	CGGCACAAAC
201	CCCTCGCTTT	GAATCCGCGC	CCGCAAAATC	CAGGAGCTTG	CAGCGCGAAG
251	ACAAAGCCTT	TGGCCGCGAC	AGCGAAATCA	GCGAGCTTGA	AAACGTAGGC
301	GCGCCGCTGG	TGCTGATTAA	CGACGCGCTC	GAAGACAGCA	ACATCAAAGG
351	TTTGAAGAAC	TCCGAAGAGC	TGCAACACGG	AGAAAACGGC	AAACCCGCGAC
401	GGAAGCAGCG	AAACAACGAC	GCTGCGGAAA	AAGTGGCCGC	AACTGCCGAC
451	ACTACGGATA	CGGTAGCGGT	TGAAAAACCG	AAACGCAGTG	CGGAACAAAA
501	ACCGCAAAAA	GCGAAACGCA	TGCGCAAAAC	CAAGCCCCAA	GCCAAAGAAA
551	CCAAACACCG	CGAAAAGTTT	GCGCGAAGAC	CGAAACATGC	CGCCGAAAAA
601	ACCAACACGG	ATACGGCAAA	ATCCGACAGC	CGGGTAAAG	AAGTCGAAAA
651	AGCCGACAG	GCTGAAGACA	AAAAAACACG	CGAAAAGAAC	AGCTTCGCGC
701	GCAAAAACAA	CGTAACGCGCA	CAAAAAACCG	ACAAAGCGGA	CAAGACCAAA
751	ACCGCGCAGA	AGGAAACATC	CGGTAAAAAA	GCGCCAAATT	AGGCAGGTTA
801	TGCGCAAAAA	GAGGCGCCT	TAGGCTTCCA	GCGCAAAATC	AAGGCGGCGT
851	GTATCGATT	GACCATCACC	GAATTATGA	CCGACAAACG	CAAAGTTTAC
901	CGCGTCAATT	CAAGCAACTA	TAAAAACGCA	AGGGATGCGC	ACACGCGATT
951	GAACAAATTG	CGGCTGACG	GATTCGCGCG	TCAGGTAAAC	AATGAATA

a746.pcp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTSACL	VVASCILLAA	ALLSSGFAEQT
51	AGETSGSEVKN	AAGAAQPTAL	KSAADVPQDL	AGEDKPSAAD	SEISEFENVG
101	APLVLLINDRL	EDSNIKGLEA	SEKLOQAETA	KTPAKQAQOR	AAEKVPFATAD
151	SDTVVAVEPK	AKTEATKPKQ	AERTAKKAPK	AKETKTAEVK	ADBKPTAAEK
201	TKFDPTAKSDS	AVKEAKKAKD	AESKATKAEK	RSDGKHETHA	QKTDKADTKT
251	TAEKESKSGK	AAIQAGYAEK	ERALSLOKMT	KAAIGDSTIT	EIMTDNGKVV
301	RVKSSXNKNK	RAIDRLNLK	RVHGIAGQOV	NE*	

Homology with a predicted ORF from *N. meningitidis*

a746/m746; 99.7% identity in 332 aa overlap

a746.pep MSENKQNEVLSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
|||||
m746 MSENKQNEVLSGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
|||||

a747/m747 97.1% identity in 102 aa overlap

a747/m80195

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR 60
+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWEVKFDLNSRYKLNTGVTLNKKDINQKTNGWGFGLGANIGKKLGESASIEAGPEYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
+T + E + GD + ++ EYG RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

```

g748.seq
1  ATGAGTCAAA ACCAACCCGC ACAACCCGACC AAACGCAATT TGTTCAAAAC
51  CGCCCTTGCC GTCGGCGCAA TCGCGCAATT CGGAGGTTAT TTCGGCGGCA
101  AAAAACAGGG CGAAACCCGC GAACGCACCG CCGAAAGCCA ACACTCGGCC
151  CAAGCCCTAT CCGTCTACGG CGAACATCAG CGAGGTTATCG TTACGCCGCG
201  GCAGCGGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301  ACCCAAGGCG GAGATACCA AGACCGCGAC GACAAACTCC CGTCAGCCGG
351  CAGCGCATG TTGGTAAAG CTTTCAACCC CGACGGATTG ACCGTTACCG
401  TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAAACGGTTT ATTTGACAGA AATTGCGACT TTCCCAACG ATAAGCTGCA
501  AAAAGCTGCG TGGCAGCGCG ATTTGAGCCT GCAAAATCTCG GCCTTCAACC
551  CCGAAACCTG CCAAACCCGC CTGCGCGACA TCATCAAAAC CACCGGCCAA
601  ACCCGCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651  CGCGCGCATG GCGGCGCGCA ACCTGTTGGG TCTCCGAGAC GGCACGGGCA
701  ACCCCAAGGT TTCCGATCCC AAAACCCGCG ACGAGGTTTT ATGGACGGCG
751  GTGGCGGCCA ACAGCCTTCA CGAACCCGAG TGGGCGAAAA ACGCGAGCTA
801  TCAGGCACTG CGCCTTATCC GCGCCTTTGT CGAGTTTGGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAAT CACGGGGGCG
901  CCGATGGAGC GCAAAAAAGA AGCCGACCAA CCGGATTTCC CCAAAGACCC
951  CGAGGGTGAT ATCAGGCCA AAGACGCECA TATGCGCTCG GCGAATCCGC
1001 GCGATCCCGA ATTCTTCAA AAACACTGCC TCTTCGCGCG CGCCTACAGC
1051 TATTTCTCGG GACCCGCCTC AAGCGCAGCG CTTGATGTGC GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAAAT TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCCCT CGCGGCGGCG
1201 TATTTCTTTC TCTTGGCCGG CGTGGGAAAA GCGCGATTCT TGGGACAAGG
1251 GCTGCCGGCG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTLA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHO	AGIVTPROAF	SIMCAFDVTA	QSAQLENLF	RTLTRAHSIF
101	TQGGEYQDGD	DKLPSAGSGI	LGKAFNPDGL	TVTVGVGSSL	FDGREGLRDK
151	KTVHLQEMRD	FPNDKLOKSW	CGDGLSLQIC	ATGPETCQTA	LRDIHKHTAQ
201	TAVIRWSIDJ	WQPKSEFGAM	AARNLLGFRD	GIGNPKPVSD	TADEVLWTG
251	VAANSLDDEP	WAKNGSYQAV	RLIRRFVEFV	DRTPLQEQT	IFGRRKYSGA
301	PMDGKKEDAQ	PDFAKDPEDG	ITPKDGHMRL	ANRPDEFLK	KHCLFRRAYS
351	YSRGPASSGQ	LDVLGVFVCY	QANLADGFI	VONLLNGEPL	EYISYFPFGG

g748	AFTPETCQTALRDIIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP	190	200	210	220	230	240
m748.pep	KTAEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFIGRRKYSGA	250	260	270	280	290	300
g748	KTAEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRRFVEFWDRTPLQEQTDFIGRRKYSGA	250	260	270	280	290	300
m748.pep	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ	310	320	330	340	350	360
g748	PMDGKKEADQPDFAKDPEGDITPKDSHMLANPRDPEFLPKKCLFRRAYSYSRGPASSGQ	310	320	330	340	350	360
m748.pep	LDVGLVFVCYQANLADGFI FVQNLLNGEPLLEYISPFGGGYFFVLPGVGKGGFLGQGLLG	370	380	390	400	410	420
g748	LDVGLVFVCYQANLADGFI FVQNLLNGEPLLEYISPFGGGYFFVLPGVGKGGFLGQGLPG	370	380	390	400	410	420
m748.pep	VX						
g748	VX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2565>:

```

a748.seq
1      ATGAGCAAAA  ACCAACCCGC  ACAACCGACC  AGGCGCACTC  TTTTAAAAAC
51     CGCGATCGCA  GCTGGAGCAG  TCGGCGCAAT  CGGAGGTTAT  CTCGCGGCAC
101    AAAAACGGGG  CGAAACCGCC  GAACGACACG  CCGAAAGCCA  ACATCGCCCC
151    CAAGCGCTATC  TCTGCTACGG  CGAACATCAG  GCAGGCACTG  TTACGCCGCC
201    GCAGGCGTGT  TCGATTATGT  GCGCCTTCGA  CGTAACCCGG  CAAAGTGCCA
251    AGCAGCTGGA  AAACCTGTTC  CGCAGCGCTA  CGCCCGCGAT  CGAGTTTCTC
301    ACCCAAGGCG  CGGAATACCA  AGACCGCGAC  GACAAAGTTC  CGCCAGCCGG
351    CAGCGGCATG  TTGGGCAACG  CCTTCAACCC  CGACGGGTTC  ACGGTTACCG
401    TGGGGGTGGG  CAGCAGCGCT  TTTGAGGGCC  GGTTCCGAGT  CAAAGACAAA
451    AAACCGATTG  ATTTCGAGGA  AATGCGCGAC  TTCTCCAACG  TAAAGCTGCA
501    AAAAAGCTGG  TGGCAGCGCG  ATTTAGGCTG  GCAAATCTGT  GCTTCTACCC
551    CCGAAACCTG  CCAAGCCGCC  CTCGCGCACA  TCATCAAAAC  CACCGTCCAA
601    ACCCGCGTTA  TCCGCTGGAG  TATCGCAGGG  TGGCAGCCTA  AATCCGAACC
651    CGGCGCGATG  GCGGCGCGCA  ACCTGTTGGG  CTTCCGCGAC  GGCACGGGCA
701    ACCCCAAGTG  TTCCGACCCC  AAATGCTCCG  ACGAGGTTTT  GTGGACGGGG
751    GTGGCCCGCA  ACAGCCTCGA  CGAACCGGAG  TGGGCGAAAA  ACGGCGAGTA
801    TCAGGCACTG  CGCTTATCTT  GCCACTTTGT  TGAGTTTGGG  GACAGGACGC
851    CGCTTCAAGA  GCAAAACGAC  ATTTTCGGGC  GGCGCAAAAT  CAGCGGCGCG
901    CCGATGGGAC  GCAAAAAAGA  AGCCGACCAA  CCGGATTTTG  CCAAGAGCCC
951    CGAGGGGATG  ACCACGCCCA  AAGACGCCCA  TATACGCTCG  CGGAATCCGC
1001   GCGATCCCGA  GTTCCTTAAA  AAACACCGCC  TCTTCCGCGC  CGCCTTACAG
1051   TATTCGCGCG  GACTCGCCTC  AAGCGGACAG  TCTGATGTCT  GGCTTGTGTT
1101   GCTCTGCTAT  GACGCCAAAC  TTTCCGACGG  ATTCACTCTC  TGCAAAAAGT
1151   TCCTCAACGG  CGAACCGCTG  GAAGAAATACA  TCAGCCCTTT  CGGCGGCGCG
1201   TATTTCTTCG  TCTTGGCCGG  CGTGAAAAAA  GCGCGCTTTT  TGGGGCAAGG
1251   GCTGCTGGCG  GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2566; ORF 748.a>:

a748.pap

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHS
51	QAYPCYGEHQ	AGIVTPQQA	SIMCAFVTA	QSAQLENLF	RTLTARIEFL
101	TQGGEGYQDG	EKLPPAGSGI	LGKAFNPDGL	TVTGVGSS	FDGRFGLKDK
151	KPIHLQEMRD	FSNDKLSQSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDT	KTADEVILWTA
251	VAANSLDEPE	WAKNGSYQAV	RLRHFFVEFW	DRTPLQEQDT	IFGRKRLSGT
301	PMDGKKEADQ	PDFAKDPEN	TPPKDSHRL	ANPRDPEFLK	KHRLFRFRRAYS
351	YSRGLASSGQ	LDVGLGVFCY	QANLADGFIF	VQNLLNGEPL	EYISPFGGG
401	YFFVLPGVEK	GGFLGQGLLG	V*		

Computer analysis of this amino acid sequence gave the following results:

1221

```

801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAGTGT ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC TCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCGGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQVN
51 DNACEPMNLT VPSGQVVFNI KNSGRKLEW EILKGVVVVD ERENIAFGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAARKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPIV DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGLGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACGC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAC
501 CAAAACTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCGCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCTGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGTGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCGGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIQVN
51 DNACEPMELT VPSGQVVFNI KNSGRKLEW EILKGVVVVD ERENIAFGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

```

m749/g749 96.1% identity in 388 aa overlap

          10      20      30      40      50      60
m749.pep MRKFNLTAISVMLALGLTACQPPEAEKAAPASGEAQTNEGGSVSIQVNDNACEPMELT
          |||||
g749      MRKFNLTAISVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIQVNDNACEPMNLT
          10      20      30      40      50      60

```

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKOV NEILAKYRTH
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVNDNACEPMELT				
m749	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVNDNACEPMELT				
	70	80	90	100	110	120
a749.pep	VPSGQVVFNIKNNNGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNNGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	130	140	150	160	170	180
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTEAVKAGDIE					
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTEAVKAGDIE					
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTHKDFETYDKLG					
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTHKDFETYDKLG					
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq
 1 GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCTG
 51 TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATccgCCGCA TCCCAAGCCG
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
 151 GTTGTGCCGA AGAATCCCGA ACgctcgcc gtgtAcgaCt ggCGGCGTt
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
 251 TGGCGGTGGA CTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
 301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
 351 TGTCAATTACC GCGGGGCGCG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
 451 GGCAGAGAAC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
 501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
 551 AAGCCGCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACAGGCAAC
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
 651 CGACATCGGC CTGCCGCGCG TGGACGAATC TTACGCAAC GAAGGGCACG
 701 GGCAGCCCGT TTCTTTCGAA TACATCAAG AGAAAAACCC CGGCTGGATT
 751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

1225

```

g750      GGPGEAEYEQAKNATTIDLTVDNGNI RTSGEKQMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
QTREAAKKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDI GLPPVDES LRNEGHGQPV SF
I |||||

g750      QKREAAKKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDI GLPPVDES LRNEGHGQPV SF
          190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYI VAGGA
I |||||

g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYI VAGGA
          250      260      270      280      290      300

m750.pep  300      310      320
RQLIQAAEQLKAAFKKAE PVAAAGKKX
|||||

g750      RQLIQAAEQLKAAFEKAE PVAAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1  GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCCGAA CCTGCCGCCG AAAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACACT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGAC AAGCGGCAA CGGTGGGGAC GCTGTTCCAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGG GCGGAAGCGT ATGAACAGTT GGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC GTTTCGCCCA AACGCGCGAA GCCGCCAAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCGGCC
601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCTGTA GACGAATCTT TACGCAACGA GCGGACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
751 TTCGACCGCG CCATCGGGCA GGAAGGGCGG GCGGCTGTCT AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCCTGC CGCGAAGTAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901 CAGGCGGCGG AGCAGTTGAA GGAGGCGTTT GAAAAGGCAG AACCCGTTGC
951 GCGGGGAAA GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1  VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDI GLPPV DESLRNEGHG QPVSF EYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVL DNAL VRGTNAWK RKQIIVMPAANY IVAGGSRQLI
301 QAAEQLEAF EKAEPVAA GK E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

```

a750/m750 98.8% identity in 321 aa overlap

          10      20      30      40      50      60
a750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAA S A S A A T L T V P T A R G D A V V P K N P E R V A V Y D W
          |||||
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAA S A S A A T L T V P T A R G D A V V P K N P E R V A V Y D W
          10      20      30      40      50      60

          70      80      90     100     110     120
a750.pep  AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGT L FEPDYEALHRYNPQLVITGGPG
          |||||
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGT L FEPDYEALHRYNPQLVITGGPG

```

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATT CACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC
651 TACCAAGTAA GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTCGATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
1  MKISRPPEFT LLQEQYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLOARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKLSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTIFYIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNAL EYVAP QD LLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATT CACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC
```


g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTGACACAGT ATTTTCCGGA AGGCTTTTGG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCCG CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTTGC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCPAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGACACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTC AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGACACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTGACACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NRMKRPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGREVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDI SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKKTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCA
101 TCTTGCTAG ACATGGATTT GAGAACATTC AGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGAAC GCACAATTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTGAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPKAEKL SKAAALIAA TAPEDRTMLR DTGDDIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGAAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGCG
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTTAGAAA GGATTGAGCC
501 ATGA

```

```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
501 TGCTTACCTC GATACCGACC GCTTCCCCTA CTTGTAGCA CTGGGTCAG
551 GCACGCAACA AGTCCGCAAA GCASACGGCA CGCGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAATAT TGGGGTTCCA
651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTCGACAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
801 CGATAATTTT TCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCCTGC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGCG GCATTGCAGT TCGACAGCAA CTCACCGTC GTCGGTAAAA
1151 ACCACACATG GCAAGGTGCA GCGGTATATG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CCGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCCGAC AGCCAGCAAA TCAACCCGA AAACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
1501 CGCCATGCGG ACGCGGCGCG GCAAATCGTC AATCACAAAC CTGACCAAGC
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCT
1601 AGTGGGTGCA ATGGGGCAAC CGTCGCGAAG GCAACGCGCG GGTTTACGAA
1651 TACATCAACC CGCACCGBAA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CGCGCGCAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
1901 AAGCAGCCAT AGAAAAAACC CGCATATCG CAAATGCCGC CGTATACGGC
1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 ACGCACCAGC AGCAGCTGTG TGCTCAACGG CGGCATGAAC CTTAAGCGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTGAGGAGC GCGCGTACCC
2101 CATGCTTACG ACCACCAGGC CAAACGCGAA CCGTTCCTTG AAAACGAATG
2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACCGCG
2351 TTTTAAAGC CGAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCGG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGCGCG ACTGACGCTT
2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTTCGGCA
2651 CATTCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAACCTGGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTTGTG AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACAAC GATACAGCCT
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTTGACG
3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
3401 CCGCGTTGC CGGCATCCGT ATGCCGAACC TGCCCGAAT GATCAGCCGG
3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGCCGGCA
3501 ACAGGCGGGA CGCCGATCG ACCGCCACCT TACCGATCCG CAGCAGCAA
3551 ACATCTGGCT GGAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
3701 AAACAACCG TTTTGATGAA GCGTATCCG CCCGAAACCG CAGCAACGGC

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCTGCG GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCACCG TGTTCGCCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTG TACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGCGCGG AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGCGGCGG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGCCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGTC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGGC GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCSCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCGCGA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGCAT TGGGCAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAAATCCA TGCAGGTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFVR
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQRRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTF GSKLNNTGQA DVAGLGTDIK
351 QKAFVVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVLAD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHHKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKTR YAALGKRVME CTEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSEERSL
701 TANLRYSF*
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1237

```

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATCCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQITDITLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQOTD NKTLLSSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRST TLSAYQIERF NRYRDPFKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFERY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGGAA AGCATTTTCC TCGCGCGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCTCTCG TGCTTTATGG GCGTACCAAC GCGCGCGGTG TCATCAACAT
501 GGTCAACAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCTTGGA GACAGACGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTG AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCGAAAA CAACTACACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGCG CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTGCG GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1239

```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
          |||
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
          370      380      390      400      410      420

          430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          |||
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          430      440      450      460      470      480

          490      500      510      520      530      540
m761.pep  YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
          |||
a761      YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
          490      500      510      520      530      540

          550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          |||
a761      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          550      560      570      580      590      600

          610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSNRNKEVTTLPGFARVDAM
          |||
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
          610      620      630      640      650      660

          670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
          |||
a761      LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
          670      680      690      700

g762.seq Not yet found
g762.pep Not yet found

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGAG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
401 CACTTTTAGT TTCTAATTTT ATTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLFIFNEV TKSIMAIY PLYFFTICK YYPYSRKVII LLSLALSIYF
101 SEMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLLVSNE ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

```

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDVVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTTCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGGTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCGGCC CATGCGCGCG
551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCGGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCACTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCAGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCGGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAAAT
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGGCGCAG GAAGTCGCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAAACGG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDVVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKMSVGVQNLPLYTGGELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKMSVGVQNLPLYTGGELSGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCGCGCATT TGGAACGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCGGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTCAGG GCGGCTATGA ATGTACGGGC GGAGATTAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAESEQAF PAHLELTDPF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDQOHVKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGVEQO QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSLPQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCGCGCATT TGGAACGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGCATCGAG CAGCAGAAAA

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```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAGC
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCTT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ATATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1  MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEEQAF LPAHLELDT P
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKT VSGGRSKTI Q
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVA?DD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHTDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEEQAF LPAHLELDT PVSAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEEQAF LPAHLELDT PVSAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDI VAAASGKT VSGGRSKTI QPLETAVVKAVHVRDQHVKGGE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDI VAAASGKT VSGGRSKTI QPLETAVVKAVHVRDQHVKGGE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGT DSDVVQSEQA LQAAQLSKLR YEAVLAALES RTVPHIDMAQ ARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGT DSDVVQSEQA LQAAQLSKLR YEAVLAALES RTVPHIDMAQ ARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQH QYQAWAAQDA QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQH QYQAWAAQDA QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHA FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHA FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA QKMMVVA?DD					
a764	310	320	330	340	350	360
	LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA QKMMVVA?DD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG KVKSVSHTDAV SHEQLGLVYT					

1245

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|||||
a 764      DKMDVEVLVLNKKDIGFEVQQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pép    AVVSLDKHTLNIDGKAVNLTAGMNVTAETKTKRRVLDYLLSPLQTKLDESFRERY
              |||||
a 764      AVVSLDKHTLNIDGK
              430
```

g765.seq not yet found

g765.pép not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGCTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```
m765.pép
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FFRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDDEIAAI MGHEMTHALH ERGKNKVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLPLPTVM PVYEQSVRNK
301 GRVNKKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCCTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGCTGGG
401 CAATGCCCGG CGGGAAAATG GCGTTTTATA CGGGGATAGT CGATAAATCT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```
a765.pép
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
```

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```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGDGEIAAI MGHMETHALH EHGNKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLEEEA DEGGMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLPTVM PVYEHsVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACAVVADVYG		
a765	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACTVVADVYG		
	10	20	30	40	50	60
m765.pep	70	80	90	100	110	120
	HDSATMNAAA	KDYMKTVELNKSAGNVD	TTSRTARRVQAVFRRML	PYADAANNTSHKFDW		
a765	QDSATMNAAA	AEDYMKTVELNKSAGNVD	TTSRTARRVQAVFRF	PYADAANNTGHHKFDW		
	70	80	90	100	110	120
m765.pep	130	140	150	160	170	180
	KMTVFKNDEL	NAWAMPGGKMAFYTGIV	DKLKLTDDEIAAIMGH	EMTHALHEHGKNKVGQ		
a765	KMTVFKNDEL	NAWAMPGGKMAFYTGIV	DKLKLTDGEIAAIMGH	EMTHALHEHGKNKVGQ		
	130	140	150	160	170	180
m765.pep	190	200	210	220	230	240
	ILTNAAQIGT	QIILDKKPDTNP	ELVGLGMDILGTYGLT	LPYSRSLEEEADEGG	MMLMAQ	
a765	ILTNAAQIGT	QIILDKKPDTNP	ELVGLGMDILGMYGIT	LPYSRSLEEEADEGG	MMLMAQ	
	190	200	210	220	230	240
m765.pep	250	260	270	280	290	300
	AGYHPAAAVR	VWEKMNQENDQNGFI	YAITSTHPTNNARIEN	LKRLPTVMPVYE	QSVRNK	
a765	AGYHPAAAVR	VWEKMNQENDQNGFI	YAITSTHPTNNARIEN	LKRLPTVMPVYE	HSVRNK	
	250	260	270	280	290	300
m765.pep	310					
	GRVNKKRRRX					
a765	GRVNKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGCCG GAAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTGATC CCTTTGTTA1 TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTTGAAAT ATCAGGCCAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAAATCCGT TTGGAAAAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAAGTATGTC GCGCCTATGA TTCCTCCGAA
451 GCTGCCGCCG TCGCATTAAG AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLsAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEF*G
51  YFCVHCHHFD PLLKLGLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

```

1247

```

101 GLKYQANSV FKAVYEOKIR LENRAVAGKW ALSQKGFQDGK KLMRAYDSPE
151 AAAVALKMQK LTEQYQIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

```

m767.seq
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGTCG GGTAATAATTG AGGTTTTGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGGAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCCTATGA TTCCCGCGAA
451 GCTGCGCGCG CCGCATTAAT AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCAGC CCGACCGTTA TTGTCGCGCG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTCGCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

```

m767.pep
1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51 YFCVCHHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAANLS
101 GLKYQANPAV FKAVYEOKIR LENRSVAGKW ALSQKGFQDGK KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

```

m767/g767      95.8% identity in 214 aa overlap

              10      20      30      40      50      60
g767.pep      MKFKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVCHHHFD
              |||
m767           MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVCHHHFD
              10      20      30      40      50      60

              70      80      90      100     110     120
g767.pep      PLLLKLKALPSD TYLRTEHV VWRPEMLGLARMAA AVKLSGLKYQANS AVFKAVYEOKIR
              |||
m767           PLLLKLKALPSDAYLRTEHV VWRPEMLGLARMAA AVNLSGLKYQANPAV FKAVYEOKIR
              70      80      90      100     110     120

              130     140     150     160     170     180
g767.pep      LENRAVAGK WALSQKGF DGKKLMRAYDSPE AAAVALKMQKLTEQYQIDSTPTVIVGGKYR
              |||
m767           LENRSVAGK WALSQKGF DGKKLMRAYDSPE AAAAALKMQKLTEQYRIDSTPTVIVGGKYR
              130     140     150     160     170     180

              190     200     210
g767.pep      VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              |||
m767           VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
              190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

```

a767.seq
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AAAACAGTCG GGCAAAATTG AGGTTTTGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAATGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCGGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGAATAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAATGATGC GCGCCTACGA CTCTCTCTCG

```

1248

```

451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
51  YFCVHCHHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767 96.7% identity in 214 aa overlap

      10      20      30      40      50      60
a767.pep MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQKSGKIEVLEFFGYFCVHCHHFD
m767      MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQKSGKIEVLEFFGYFCVHCHHFD
      10      20      30      40      50      60

      70      80      90     100     110     120
a767.pep PLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFYAYEQKIR
m767      PLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFYAYEQKIR
      70      80      90     100     110     120

      130     140     150     160     170     180
a767.pep LENRSVAEKWALSQKGFDDGKKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR
m767      LENRSVAGKWALSQKGFDDGKKLMRAYDSPAAAAALKMQQLTEQYRIDSTPTVIVGKRYR
      130     140     150     160     170     180

      190     200     210
a767.pep VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
m767      VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGCTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQSAVWI DVRSEQEFSE
51  GHLHNAVNIPIVDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHHGGY EDLLKKGMMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGCTCAAC CTCTACTGCC

```

1249

```

251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGGCCTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

```

m768.pep
1  MNIKHLITAA LIA^AAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMMK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

```

m768/g768 96.6% identity in 119 aa overlap

              10      20      30      40      50      60
g768.pep  MNIKQLITAALIASAAFATQAAPQKPVSAQAQHSASVWIDVRSEQEFSEGHLEHNAVNI P
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m768      MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHSASVWIDVRSEQEFSEGHLEHNAVNI P
              10      20      30      40      50      60

              70      80      90      100     110     120
g768.pep  VDQIVRRIYEAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m768      VDQIVRRIHEAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

```

a768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
101 AACATTACAG CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCGG
201 CATAACAGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
301 TATACGAATG TTGCCAATCA CGGCGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

```

a768.pep
1  MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSASVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMMK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

```

m768/a768 99.2% identity in 119 aa overlap

              10      20      30      40      50      60
a768.pep  MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHSASVWIDVRSEQEFSEGHLEHNAVNI P
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m768      MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHSASVWIDVRSEQEFSEGHLEHNAVNI P
              10      20      30      40      50      60

              70      80      90      100     110     120
a768.pep  VDQIVRRIHEAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m768      VDQIVRRIHEAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKKGMMKX
              70      80      90      100     110     120

```

1250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATATGCC
51  TGCACGAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCCG ATTGTGTGCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCGG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTCCCATT ACCGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAGC GCGGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGCCCGG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGCGGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGCG GCACGCCTTT ATTTCAACCG TTGGCAAAAC AGAGATGGC
1001 AACCGCTGTC TTCGGCGGAG TGGGGCGCTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCCGACA ATACCCATTT GCAAATTCTC AATTGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCGCGCGA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCTTG TCTTCGCTGT TCGGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCTG CTTCTTCAGC AGTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCGG CGCCTGACGC TGTCGCAACG
1401 CGAAACGTGG AGCAACGATG TGTTAAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGVVLQVDGE TLLKNPELLS RAMYSVVSN
101 NIAGIRVILP IYLQARQDK MLALYAOGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPLQ MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNWRQT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQEWGSGSL SSLFRLGVAK RHYEKPFFFS SFKGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCAACCGG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGCAGGT
201 CGGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CGGCCGTCG TATGCGTTTG GCGGCAGCAT TGTGTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCG GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AATGGAATT
701 TCCCGAAACA GGTGGACGCG ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGCGGCA CGCCTTTATT TCAACCGTTG GCAACCCCG AAATGCAAA
1001 CGTTGTCTTC GGCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTTGCA AATTTCGAAT TCCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCGCACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCGA CGGCTGTCT TCCTGTTGCG GCCTCGGCGC

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1251

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1251 GGCAGAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPGQVREK GKVLOIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKQQYQ KWTFFPKQVDG TAVNYRLGAE
251 KWSLKNWYGT TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYTG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKN:RRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GGEWGGGSLG SLLRLGAAKR HYEPGFFSFG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI					
m769	LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPI					
	10	20	30	40	50	
g769.pep	60 DREKVPQVREKGVLOVDGETI IYNPEL SRAMYSAVVSNNIAGIRVILPIYLQQAQQD	70	80	90	100	110 119
m769	60 DREKVPQVREKGVLOVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD	70	80	90	100	110
	60	70	80	90	100	110
g769.pep	120 KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD	130	140	150	160	170 179
m769	120 KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD	130	140	150	160	170
	120	130	140	150	160	170
g769.pep	180 RLKTEDLPPOLMEQVELYRKALRERDAWKVNGGFSVTREHNIHQAPKQQYGNWTFPKQV	190	200	210	220	230 239
m769	180 RLKAENLPPOLMEQVELYRKALRERDAWKVNGGFSVTREHNIHQAPKQQYGNWTFPKQV	190	200	210	220	230
	180	190	200	210	220	230
g769.pep	240 DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV	250	260	270	280	290 299
m769	240 DGTAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA	250	260	270	280	290
	240	250	260	270	280	290
g769.pep	300 GLAVFHERRYTGNDAYSANGARLYFNRWOTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI	310	320	330	340	350 359
m769	300 GLAVFHERRYTGNDAYSYTNGARLYFNRWOTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI	310	320	330	340	350
	300	310	320	330	340	350
g769.pep	360 SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGGEWGGGSLSLRLGVA	370	380	390	400	410 419
m769	360 SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGGEWGGGSLSLRLGAA	370	380	390	400	410
	360	370	380	390	400	410
g769.pep	420 KRHYEPGFFSSFFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE	430	440	450	460	470 479
	420	430	440	450	460	470

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m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAVFVEFNKTFX
          |||||
m769      KNRAVFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTFTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCTATGCCC
101 AAGAACACCC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAGAA GGAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCAACAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATACG GGAATTGAT TGTGCGCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTT GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG CGGCGGACGT
801 GTCCGCGCAG GTTTATCCGG GGAATAAGAA ATCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GGCGCAAAGA TGGCGGGCTG
901 GCAGTGTTCG ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGCCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCGACCGG GGGCGCAAT TTCAACCGTT ACGGCGTGGC CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 CCGAAACGG CTTATGAAA AACCCGGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CTTGAGCCT TTGGCACCGG
1351 RERDAWKQIS SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
1401 AQEWGSGSL SLRLGAAKR HYEKPFFSG FKGERRDKE LNTSLSLWHR
1451 ALHFKGITPR LTLSHRETRS NDFNEYEKN RAFVEFNKTF *

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAEETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADOFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNNI NQAPKRQOYG KWTFPKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
401 GQEWGSGSL SLRLGAAKR HYEKPFFSG FKGERRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLPLLASAAYAEETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLPLLASAAYAEETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQQDKM

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m769      |||
           EKVPGQVREKGV LQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDDKM
           70      80      90      100     110     120

a769.pep   130      140      150      160      170      180
           LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           |||

m769      LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           130      140      150      160      170      180

a769.pep   190      200      210      220      230      240
           KAENLPFQLMEOVELYRKALRERDAWKVNGGFSVIREHNNINQAPKROQYGKWTFFPKQVDG
           |||

m769      KAENLPFQLMEOVELYRKALRERDAWKVNGGFSVIREHNNINQAPKROQYGKWTFFPKQVDG
           190      200      210      220      230      240

a769.pep   250      260      270      280      290      300
           TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           |||

m769      TAVNYRLGAEEKWVSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           250      260      270      280      290      300

a769.pep   310      320      330      340      350      360
           AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLNTRRARSNDNTHLOISN
           |||

m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLNTRRARSNDNTHLOISN
           310      320      330      340      350      360

a769.pep   370      380      390      400      410      420
           SLVFYRNARQYWMGGLDIFYRERNPADRGDNFNRYGLRFAGWQEWGGGSLSLRLGAAGR
           |||

m769      SLVFYRNARQYWMGGLDIFYRERNPADRGDNFNRYGLRFAGWQEWGGGSLSLRLGAAGR
           370      380      390      400      410      420

a769.pep   430      440      450      460      470      480
           HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
           |||

m769      HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
           430      440      450      460      470      480

a769.pep   490
           RAFVEFNKTFX
           |||

m769      RAFVEFNKTFX
           490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTGACGCA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCGTGCGC CAAACCGAAA
301 GAAGTTTTC ACGCGGTAC GGGCTTCGGC TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSRIQVRYV DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

      10      20      30      40      50      60
g770.pep MNRLLLLSAAVLTACGSGETDKIGRASTVFNMLGKNDR IEVEGFDDPDVQGVACYISYA
          |||||:|||||:|||||:|||||:|||||:|||||
m770     MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR IEVEGFDDPDVQGVACYISYA
          10      20      30      40      50      60

      70      80      90     100     110     120
g770.pep KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKRGTGFQFVSRQIVRYY
          |||||:|||||:|||||:|||||:|||||:|||||
m770     KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKKEVFKHGASFAFKSRQIVRYY
          70      80      90     100     110     120

      130     140     150     160     170     180
g770.pep DPKRKAFAFYLVSQKIVQSPKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
          |||||:|||||:|||||:|||||:|||||:|||||
m770     DPKRKTFAFYLVSQKIIQSPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
          130     140     150     160     170     180

g770.pep KNPDKRX
          :| ||||
m770     ENLDKRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACCAGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRK*
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASF AFKSRQIV RYY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASF AFKSRQIV RYY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGS PKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGS PKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPDKRX					
m770	ENLDRKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGTGACG	ATGCTGCTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCGGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGCGCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAT	CGGATTGAGC
301	TGGA AAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTCTGCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGAGAAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCTTTTC	AGACGGCATC	GGCAGGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TCCGCAACC	TCCACCTGAC
801	CGCGCAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAAACCAAT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGAGATC	GGGACAACGG	GCTGGACGCC
1051	CGCGCCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCGTTGGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGGCGCA	CCGCACCTCG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAACC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCTCCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGCGCG	CATCAGCATC
1501	GCCCAACACC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

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1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTCAACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAAAC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRKISFD ADIRRRRLPR PTVILKNLTI TEPDGGRVAV SVVETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSAFVNRII
151 VDNSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLFVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNNSI KGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQWNNAEL NGTFDRQPVV
401 AKFKYTREGA PHLEAAAAAQ KLNLAAPYLDE FRQNGKIFP DILGRLSGNV
451 EAHKIGISIQ LPGLQLDDME TYLHADKDH I ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLASGENRK
551 QLIRSLOGSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 FLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPREP
701 *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCGAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCGCTGAA AACATCCGCA GCCGCTTACA ACAAAGCATT
151 GCACACACAC ACCGGAATAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCGTACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAAAC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AACGCCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTGCTCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GCGCGCGCGG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCGTGGA CGGACACGGC ATTACCATT
701 CCACCCACCG CAGCCCTTCT GTCCGCTTCA ACGCGGCGGG AGCGGATGCG
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCGCAACCC TCCACCTGAC
801 CGCCCAAAAT CCGCGCGTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGCGGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCGGCTC GTATGGACGG AAAACAAAGG GCTGGACGG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 CGAAATTTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAAATCG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTCA AGGGCTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 CCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTTCAT GACCTGACCG CCGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCAAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCACACAGC AAATTTGAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTTACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTTC CGCAAAGAGA
2051 AACAGAAAAA CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAA
2101 CCTAAAGAAC CGTA

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1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
 51 ANTHRRKISFD ADIQRRLPR PTVILKNLTI TEPGGDOTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWWVSSAE LALTRDGKGV WHIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNNNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
 451 EAHKIGKGVQ LPGLQLDDME TYLHADKGGH ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTFFHFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKPEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap
	10 20 30 40 50 60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIANTHRRKISFD
m771	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIANTHRRKISFD
	10 20 30 40 50 60
	70 80 90 100 110 120
g771.pep	ADIRRRLLPRETVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWWVSGAD
m771	ADIRRRLLPRETVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWWVSGAD
	70 80 90 100 110 120
	130 140 150 160 170 180
g771.pep	LALTRDRNGAWNIDQLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEISLNLQSPDSS
m771	LALTRDRNGAWNIDQLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEISLNLQSPDSS
	130 140 150 160 170 180
	190 200 210 220 230 240
g771.pep	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
	190 200 210 220 230 240
	250 260 270 280 290 300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
	250 260 270 280 290 300
	310 320 330 340 350 360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDGLDAPRLHISTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDGLDAPRLHISTLQD
	310 320 330 340 350 360
	370 380 390 400 410 420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNNNAELNGTFDRQPVAAKFYKTREGAPHLEAAALQ
m771	TVDRLPQPRFISRLDGSLSIPNLQNNNAELNGTFDRQPVAAKFYKTREGAPHLEAAALQ
	370 380 390 400 410 420
	430 440 450 460 470 480
g771.pep	KLNLPYLDVFRQONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH
m771	KLNLPYLDVFRQONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH

1258

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          430      440      450      460      470      480
          490      500      510      520      530      540
g771.pep  ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI
          |||||
m771      ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI
          490      500      510      520      530      540

          550      560      570      580      590
g771.pep  DLTAGSENRRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT
          |||||
m771      DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMNLKNGISGKTADNAAPSTPFHRT
          550      560      570      580      590      600

          600      610      620      630      640      650
g771.pep  LNSEISDGISRHHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG
          |||||
m771      LNSEISDGISRHHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG
          610      620      630      640      650      660

          660      670      680      690      700
g771.pep  TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPK~PX
          |||||
m771      TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX
          670      680      690      700

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGTCTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAAGCATT
151  GCCCATACGC  ACCGAAAAAT  CTCGTTGAT  GCGGATATAC  AGCGCAGGCT
201  TCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCAT  ACCGAACCCG
251  GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351  GAGTCGGGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAAACATCC
401  AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAAACA  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501  GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551  TTGAAAGTTC  GGGCATACTG  GTTGGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701  CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCCCAAAAT  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851  CCGTCAACGG  CGCATTTACC  GCCGGCGGCG  AATATGCCCA  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001  TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051  CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101  ACCCGTTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCCTTGCC
1201  GCGAAATTCA  GATACACACA  TGAAGACGCA  CGCATCTGG  AAGCCGCCGT
1251  CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301  AAAACGGCAA  AATATTTCCC  GACACCCTCG  CCAAGCTGTC  CGCGGACATC
1351  GAGGCGCACC  TGAAATCCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451  GTTTCAAGTC  AGGGCTTTAC  GCGGGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  CGCGGTCATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651  GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGTAAATA  TTTCCAACGG
1701  TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTTCG
1751  GCAAAACTGC  CGACAATGCC  GCACCCAGCA  CACCCCTCCA  CCGATTACG
1801  CTCACAGCG  AAATTTCAGA  CGGCATCAGC  CGGCACATCG  ATACCGAACT
1851  CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901  CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951  AACAAACCGA  TTCCCTGAA  AATCACCGGT  ACGGTGGACA  AACCCTCCAT
2001  TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCC  CGCAAAGAGA
2051  AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACATGGCA  GTGGCTCAA
2101  CCTAAAGAAC  CGTAA

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This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep

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1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGQLDDME TYLHADKGI ALSRFKSGLY GGHTGGGSI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLOGSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLEQKJWLK
701 PKPE*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPE	NIRSRLQOSIAHTHRKISFD				
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPE	NIRSRLQOSIAHTHRKISFD				
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
m771	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	WKNLWSDQIQIEKVVVSSAE				
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS				
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS				
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFSLDGI	GTPKISPFHFEASTSLDGHGITISTTGSPS				
m771	GQPFESSGILVWGKLSVPWKSRLGLFSLDGI	GTPKISPFHFEASTSLDGHGITISTTGSPS				
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTALARNNSI	KIETVNGAFTAGGEYAQWDG				
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALARNNSI	KIETVNGAFTAGGEYARWDG				
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD				
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQT	VAAKFRYTHEDAPHLEAAVALQ				
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQT	VAAKFRYTHEDAPHLEAAVALQ				
	430	440	450	460	470	480
a771.pep	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQDDMETYLHADKGI				
m771	KNLNTPYLDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQDDMETYLHADKGI				

1260

	490	500	510	520	530	540	
a771.pep	ALS	RFK	SGLYGGHTEGGIS	IAN	TRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI		
m771	ALS	RFK	SGLYGGHTEGGIS	IAN	TRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI		
	490	500	510	520	530	540	
	550	560	570	580	590	600	
a771.pep	DL	TAGGETR	KELIRS	LQGSLS	LNISNGAWHGIDMDN	ILKNGISGKTADNAAPSTPFHRFT	
m771	DL	TAGGETR	KELIRS	LQGSLS	LNISNGAWHGIDMDN	ILKNGISGKTADNAAPSTPFHRFT	
	550	560	570	580	590	600	
	610	620	630	640	650	660	
a771.pep	LN	SEISD	GISR	RHIDTEL	FSDSLYVTSNGYTNLDTQELSEDV	LIRNAVHPKNKPIPLKITG	
m771	LN	SEISD	GISR	RHIDTEL	FSDSLYVTSNGYTNLDTQELSEDV	LIRNAVHPKNKPIPLKITG	
	610	620	630	640	650	660	
	670	680	690	700			
a771.pep	TV	DKPSIT	VDYGR	LTTGGINSR	KEKQKILED	TLLQWQWLKPKEPX	
m771	TV	DKPSIT	VDYGR	LTTGGINSR	KEKQKILED	TLLQWQWLKPKEPX	
	670	680	690	700			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTT	CGGCA	CGGTCTT	GCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTGCG	GCGTTGGCGG		
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC		
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACTGCGGAA	TCGATTTTCG		
201	GCGCGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG		
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CGGTAGTCGT	TGCTTTTCGG		
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT		
351	CGCGGACATC	GTCCGCTACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG		
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCCCTG	AGATGCCGTT		
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA		
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCCAT	TTCCGACAACG		
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC		
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA		
651	CAATATCGCC	GATAATCCGC	GTGTCTTGCA	AAAAATTCTG	CCCGAAACGC		
701	TTGCGGGCTT	TGTGTTCTTT	CATCGTGTGT	CCTCTTCGGT	TGAAACCCCG		
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGCGGGGCG	GTAACCCCTT		
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCT	TCCTGTGTGT		
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCCGC	ATTGTAA		

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VF	GT	VL	LR	TD	DC	LQ	II	VG	K	FF	QV	V	Y	G	F	A	AL	AE	GE	F	H	Q	F	G	EM	IE	IV	RL	LA			
51	DT	VF	HR	NH	AH	H	CG	ID	FRR	GI	E	R	F	GR	HV	NQ		LH	IE	KI	LQ	HH			TQ	AT	VV	V	A	F	R		
101	RG	NH	AL	DH	FF		LQ	KV	HIG	DI	V	R	HL	RQ	FE	Q		RR	GD	VI	RQ	VA			DD	FL	F	A					
151	EI	KL	Q	H	V	A	F		NH	OF	I	R	K	R	Q	R		F	O	T	A	Y	D	V	A	V	D						
201	RA	DF	NH	DI	IR		L	R	A	H	G	V	D	N	I	A		D	N	P	R	V	L	Q	K	I	L	P	E	T	L	A	G
251	P	F	R	A	A	G	S	D	S	V		W	A	G	R	N	P	F	Q	I	R		T	H	R	A	V	L	Y	S			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTT	CGGCG	CGGTCTT	GCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTGCG	GCGTTGGTGG		
101	AAGGCGAGTT	TCACGAGTTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC		
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTCG		
201	GCGCAGGATC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG		
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CGGTAGTCGT	TGCTTTTCGG		
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGACGATA	AAGTGCATAT		
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA		
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCCCTG	CGATGCCGTT		
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA		
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCCAT	TTCCGACAACG		
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC		
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA		
651	CAATATCGCT	GATAATCCGC	GTGTCTTGCA	AAAAATTCTG	CCCGAAACGC		

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIEKILQHH AQAADVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEOK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGVFVF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVYS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

```

m772/g772      85.2% identity in 298 aa overlap

              10      20      30      40      50      60
g772.pep      VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAH
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772          MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

              70      80      90      100     110     120
g772.pep      HCGTDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772          DGGIHFRRRVVERFGRYVNOHFHIEKILQHHAAQAADVVAFRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

              130     140     150     160     170     180
g772.pep      VRHLRQFEQRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRQRQFQTAYDVAVD
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772          VRHLRQLEQKRCGNVVREVAADDFLACDAVEIKLQYIAFVNHQFIRKRQRQFQTAYDVAVD
              130     140     150     160     170     180

              190     200     210     220     230     240
g772.pep      FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGVFVF
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772          FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGVFVF
              190     200     210     220     230     240

              250     260     270     280     290     299
g772.pep      HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLVSSCVLEHKCVYSIRLMSALX
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
m772          HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATAACGATG CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAAATCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIHFRRGV ERFGRHVNQH FHIEEILQHH AQAQVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNNDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772    95.6% identity in 298 aa overlap

          10      20      30      40      50      60
a772.pep    MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
              |||
m772         MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              |||
          10      20      30      40      50      60

          70      80      90     100     110     120
a772.pep    DGRIHFRRGVVERFGRHVNQHFIHIEEILQHHQAQVVAFRGNHTIDHFFLQHKVHIDDI
              |||
m772         DGGIHFRRRVVERFGRYVNVQHFIHIEKILQHHQAQVVAFRGNHTLDHFFLQHKVHIDDI
              |||
          70      80      90     100     110     120

          130     140     150     160     170     180
a772.pep    VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              |||
m772         VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              |||
          130     140     150     160     170     180

          190     200     210     220     230     240
a772.pep    FDNVQAVQLFRQRFGNRRQRTDFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
              |||
m772         FDNVQAVQLFRQRFGNRRQRTADFNNDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF
              |||
          190     200     210     220     230     240

          250     260     270     280     290     299
a772.pep    HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
              |||
m772         HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
              |||
          250     260     270     280     290
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTGCGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAAGTTGGCA
301 ACGGGTGTGA AAAGTTCCCT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCTGTGCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTAC CTAAAAATTT TAAAAATTTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAAGTCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLTPK TADVQRNLS QSEVGKWK GIEGQMPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDQT TARLSKPEQL YSTMKGVIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAGT
201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAACTCG ACGACGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTGGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAAGTGT GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDRLKLE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAGT
201 GGAACCTTAA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACGCAA GTTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGCAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCTGAAGCCA TGTTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEL NGKVKALEHA KTHSSGRAYV QKLDRLKLE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

```

      10      20      30      40      50      60
g774.pep MKTKLPLFIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDRLDYLEGKI
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m774      MKIKLPLFIWLSVSASCASVSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI
      10      20      30      40      50      60

      70      80      90     100     110     120
g774.pep VRLSNEVEMLNKVKALEHTKIHFEGRTYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQN
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m774      VRLSNEVETLNKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQN
      70      80      90     100     110     120

      130     140     150     160     170     180
g774.pep LYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQRSMYLLQSRARMGNCESVIEIGGRY
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m774      LYNQALKHYKSGRFSAAASLLKGADGGDGGGSAQRSMYLLQSRARMGNCESVIEIGGRY
      130     140     150     160     170     180

      190     200     210     220     230
g774.pep ANRFKDSPTAPEVIFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARAAAARVRKRX
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m774      ANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARAAAARVRKRX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

```

a774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCCG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACCTCG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATACT GTCCAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTCTGCG CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TCGGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACCC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGCG
701 CCGTGCAGAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

```

a774.pep
1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNKVKALEH AKTHPSSRAY VQKLDLDRKLK
101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQOKDI ARATWRSLIQ TYPGSPAAR AAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

```

      10      20      30      40      50      60
a774.pep MKTKLPLFIIWLSVSAACSSPVSRIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m774      MKIKLPLFIWLSVSASCAS-VSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK
      10      20      30      40      50

```

1265

		70	80	90	100	110	120
a774.pep		LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD	DDRKLEKHYLNT	EGGSSASAHTVETAQ			
m774		IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD	DDRKLEKHYLNT	EGGSSASAHTVETAQ			
	60	70	80	90	100	110	
		130	140	150	160	170	180
a774.pep		NLYNQALKHYKSGRFSAAASLLKGADGGDGG	SSIAQRSMYLL	LLQSRARMGNC	ESVIEIGGR		
m774		NLYNQALKHYKSGKFSAAASLLKGADGGDGG	SSIAQRSMYLL	LLQSRARMGNC	ESVIEIGGR		
	120	130	140	150	160	170	
		190	200	210	220	230	239
a774.pep		YANRFKDSPTAPEAMFKIGECQYRLQQDIARAT	WRSLSIQTPG	SPAAKRAAAV	RRKRX		
m774		YANRFKDSPTAPEAMFKIGECQYRLQQDIARAT	WRSLSIQTPG	SPAAKRAAAV	RRKRX		
	180	190	200	210	220	230	

q790.seq not found vet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2671>:

```
m790.seq
1 ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51 ACGTTTCGGT CATCGTGCCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGCTGTGTAATCACTGCGCTTAAACATG GAAACCAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTTCGCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGCA CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT CGTGAACAG CGTGTAAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGC CAGGTTCAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCCA TACGACCATA AACTCAATC
401 ATACGCATAC GCACAACCAAC AGCGATCCG ATGGCAAAGC AGCTTCGATG
451 AGGCTCACAC CCGTCTCTTT GTTGTACAGC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAATCAACGG GCAGTTTCCGA CCTGTTTGCT TCGGTGgTGC
551 CCCCCTCGCA GTACACGTTT CCGCTTGCCA TGCCGACAC GTCCATGTCG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACCAAG CCGCTGGTGC
701 TCGCGCACCT TGTATTCGAT ATGCGGGCA GGAATGCTGAT TTATCAGAGC
751 GGCAGGCCGT GCAAGCCTT TGACGTCGCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAAC ACGGTTTATG TCCGCGGCAC AGGCAAGAA
851 GCGTGTGTAT TCGGATTACC GCCCTGATG GTGGGACGGT TGGTATGAT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTCGATTTTT GCGAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCTGGTGGC AAATCGGAAC AACCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

m790.p	1	MARRSKTFEE	AAAEVEERFG	HRGIKLVEFE	GTAKPCVINC	PKHGNQTCRS
51	YSNMFTGSSW	GCPCSCNEQA	AKAGIATLRK	NHIALEMLKQ	AVTGMTKQER	
101	ITQAYNEMT	KSVAGSNSIV	LNDVQGDFTI	NNHHTHTHHN	SDADGKALSM	
151	RIITPRLLSD	RQAAAFARTG	KLTCGSFDLFA	SVVAPSYQTF	AVAMPDTSMS	
201	PVIEKGDLLV	VEPRMCPADE	DIALIELSDK	RLVVAHLVLD	IAGRMLIYQS	
251	GRPSEAFDLP	EGSTILGVLV	ESKNGLCPPI	RQEGVLTRIT	APDVVTWGM	
301	SASKTSCSTR	TAAKSAVCFE	LRKQWATRGI	PKTRSARNPN	NA*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

a790.seq

1	ATGGCAAGAA	GGTCAAAAAC	ATTGAAAGAA	GCTGCTGCTG	AGGTTGAGGA
51	ACGTTTCGGT	CATCGTGGCA	TTAAGTTGGT	CGAGTTTGAG	GGTACAGCCA
101	AGCCGTGTGT	AATCAACTGC	CCTAAACATG	GAACACCAAC	CTGTTTCGAGG
151	TACTCCAATA	TGTTCATAGC	AAGTAGCTGG	GSTTGGCCCT	CTTGTGTTAA
201	TGAGCAAGCT	GCAAAAGCCG	GATATGCGAC	CCTTAGGAAG	AATCAGATAG
251	CGTTAGAAAT	GCTGAAACAG	GCTGTAAACG	GTATGACCAA	GCAAGAGCCG
301	ATCAGACGCG	AGCGCTACAA	TGAGATGACC	AAATCCGTGG	CAGGTTCAAA
351	CAGCATAATC	CTTAACGATG	TCCAAGGCCA	TACGACCATC	AACAACCATC
401	ATACGCATAC	GCACAACCC	AGCGATGCCG	ACGGCAAGCG	ACTGTCGATG
451	AGGCTCACAC	CCCGCTCTTT	GTGTGACAGC	CGTCAGCGCG	CGCCTTTCCG
501	CCGTACAGCG	AAACTCAGG	CGAGTTTCGA	CCTGTTTGCT	TCGGTGGTCTG
551	CCCTTTCACA	ATATACGTTT	CCCGTGTGCA	TGCCCGAGC	TCCATATCTG
601	CCGGTTATCG	AAAAGGGGGA	TTTGCTGGTG	GTCGAGCCGC	GTATGCGCGT
651	TGCGGACGAA	GACATCGTAT	TGATTGAATC	GTCGCGAAG	CGCGTGCTCG
701	TCGCGGACCT	TGTTATCGAT	ATTGCGGGCA	GGATGCTGAT	TTATCATGACG

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```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTG GAGTCAAAAA ACGGTTTATG TCCGCCGAC AGGCAAGAAG
851 GCGGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTT CTTTCGATTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTOAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
151 RLTPRPLLSR RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

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a790/m790    98.2% identity in 342 aa overlap

      10      20      30      40      50      60
a790.pep  MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||
m790      MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||

      10      20      30      40      50      60
a790.pep  MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||
m790      MARRSKTFEEAAAEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCSSRYSNMFIGSSW
          |||

      70      80      90     100     110     120
a790.pep  GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTOAYNEMTKSVAGSNSII
          |||
m790      GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTOAYNEMTKSVAGSNSIV
          |||

      70      80      90     100     110     120
a790.pep  GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTOAYNEMTKSVAGSNSIV
          |||
m790      GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER ITTOAYNEMTKSVAGSNSIV
          |||

      130     140     150     160     170     180
a790.pep  LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||
m790      LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||

      130     140     150     160     170     180
a790.pep  LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||
m790      LNDVQGDTTI NNHHTHTHNN SDADGKALSM RLTPRPLLSR RQAAAFARTG KLTGSFDLFA
          |||

      190     200     210     220     230     240
a790.pep  SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID
          |||
m790      SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID
          |||

      190     200     210     220     230     240
a790.pep  SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID
          |||
m790      SVVAPSQYTF AVAMPDTSMS PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID
          |||

      250     260     270     280     290     300
a790.pep  IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||
m790      IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||

      250     260     270     280     290     300
a790.pep  IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||
m790      IAGRMLIYQT GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
          |||

      310     320     330     340
a790.pep  SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790      SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||

      310     320     330     340
a790.pep  SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||
m790      SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
          |||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTAATTGTTT
51  TGGTTTGTTT TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACITTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAATAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTTG
1151 ACAGGCGCGC CTTGGGTTT CGGCGCCGAG CGGTGATATA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCCGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTTCAGACA AAACATTCAA TCGTGCCGTT TAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAAGCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTGATCGA TAAGATTTAT
1801 GACAGAGACG GCAGTTGCG CGCCCAATG CAACCTTTGG TGCGAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGGT ACGACCAACG ACAATAAGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 CGCGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791. pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TIAEAAMLAG LPKAPSAYNP IVNPERAKLR QKIYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNF D RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRRAV IRVKNNGGRW AVVQEP LLQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPKGG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQ QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRDIAAGKTG TTNDNKDAWF VGFNPVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQGGK MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPV L PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791. seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGTCGCT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCAGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC TGCATTACGAG CGGTTTGTTT GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACCGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAGAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGCGACTAA
1101 AAAGAAAAAT GTCGTATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTGCGGTTTT GCGGCCGCGG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGCGCGTTGG GCGGTGTTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACGCA AAACATTCAA TCGTGCCCTT CAGSCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCTGC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATAAGG GTTCTTCCG ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTCGG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCCTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCGCTAAC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

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1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVROE LYEKYGEDAY TQGFVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVA VVLDVTKKKK VVIQLPGRRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNNGRW AVVQEPLLOG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRAQM QPLVAGQNAQ QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLTLDN
751 SGIAPQPSRR AKEDDGGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

```

          10          20          30          40          50          60
g791.pep  MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10          20          30          40          50          60

          70          80          90          100         110         120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVGNVVS
          70          80          90          100         110         120

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFFKPFVYSAALS					
m791	AVVQEPQLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGQKGK					
m791	TTNDNKDAWFGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGQKGK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLMLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGTCCGT CTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGGCATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCTTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC ATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAT GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGCAT CGCGGCGACA GCTACCGCGG TGCGGAAATC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAAC ...
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGTTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGCTACGG CGGTACGATT
2101 CGCGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSESV EETVSYQLSG
351 LYTVDKMMPA VVLDVTRKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNNGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAIS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGRFSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	 MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
m791	 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180 GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSEKDKILELYFNQIYLGQ
m791	 GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSEKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240 RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
m791	 RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300 EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
m791	 EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360 RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVPA
m791	 RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420 VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
m791	 VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480 AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
m791	 AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540 KGMTASTVVNDAPISLPKGKPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
m791	 KGMTASTVVNDAPISLPKGKPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600 GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
m791	 GVGYAQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660 DRDGRLAQMOPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
m791	 DRDGRLAQMOPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720 TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAPVWVDYMRFALKGKQKGK
m791	 TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAPVWVDYMRFALKGKQKGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780 MKMPEGVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRJAADDEV
m791	 MKMPEGVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRJAADDEV

1272

```

              730      740      750      760      770      780
              790      800
a791.pep      RQDMQETPVLPSENTGSKQQQLDSLFY
              |||||
m791          RQDMQETPVLPSENTGSKQQQLDSLFY
              790      800

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

```

g792.seq
1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTTACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGTTGCT TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAA
401 GGGAAAGAGG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GCcgcaGACC
551 TGACCAAAAC GCAGgcggcG aaactgacgg tactcgtccc cgcgccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggtt cgccaaatta ccccaagcg aaacggactg
701 attgttcag atatgaaat gccgcctgaa ctggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

```

g792.pep
1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPK AADLTQQAA KLTVLVPAPF
201 YYSDHFKSKR LRNKTNIIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

```

m792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCTG
251 CGGCGCACGG CGCCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAA
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTT AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCGCGTCCC GGTATTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAAAC GCAGGCGGCA AAATGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CCGCAACA AAACCAATAT
651 CGTGCTCAA CGCATGGGT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

```

m792.pep
1  MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHFKSKR LRNKTNIIVLK RMGSALPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

```

              10      20      30      40      50      60
g792.pep      MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
              |||||
m792          MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMPMKQFEQEGRDVALDYP
              10      20      30      40      50      60

              70      80      90      100     110     120
g792.pep      WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRRNNSGEVKAGGSTISQQLAK

```

1273

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

```

a792.seq
1      ATGTTCCGCA  TCATCAAATG  GCTGATTGCC  CTGCCCGTCG  GCATCTTTAT
51     CTTTTTCAAT  GCCTATGTGT  ACGGCAACAT  CATTACCTAC  CGCGCCGTCG
101    CGCCCCATCG  GACTGCCTTT  ATGTGCATGC  GGATGAAAGC  GTTTGAACAG
151    GAAGGTCGCG  ATGTGCACTT  GGATTACCGC  TGGATGCCCT  ACAAACGCAT
201    TTCCACCAAC  CTGAAAAAAG  CCTGATTGTC  TTCCGAAGAT  GCGCGTTTCG
251    CGGGGACGCG  CGGCTTCGAT  TGGGGCGGCA  TTCAAACAGC  CATCAGGCGC
301    AACCGGAACA  CGCGGAAGT  GAGGGCGGGC  GGCTGCACCA  TCAGCAGGCA
351    GCTTGCCAAA  AACCTGTTTT  TAAACGAAAG  CCGCAGCTAT  ATCCGCAAAG
401    GCGAAGAAGC  GCGGATATCC  CGGATGATGG  AAGCCGTTAC  CGACAAGAAG
451    AGGATTTTTG  AACTGTATTT  AAATCAATC  GAATGGCACT  AGCGCGTTT
501    CGGCGCGGAA  GCCGCGTCCC  GGTATTTTTA  TCAATATACC  GCGCGCAAGC
551    TGACCAAAAC  CAGGGCGGCA  AAATCGACGG  CGCGCGTCCC  CGCCCGCTC
601    TACTACGCGC  ACCATCGGAA  AAGCAAAACG  CTCGCAACA  AAACCAATAT
651    CGTGCTCAGA  CGCATGGGTT  CGGCAGAGTT  GCCTGAAAGC  GACACGGACT
701    GA

```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIYT	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRSTN	LKKALIASED	ARFAGHGDFD	WGGIGNAIRR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RFELYLNSI	EWHYGVGEA	AASRYFYQIP	AAKLTQKQAA	KLTRVPPAPL
201	YYADHPKSKR	LRNKTINVL	R	SDT*	

m792/a792 99.6% identity in 233 aa overlap

a792.pep	10	20	30	40	50	60
	MFRIIKWLLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
m792	10	20	30	40	50	60
	MFRIIKWLLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
m792	70	80	90	100	110	120
	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
a792.pep	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP				
m792	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP				
a792.pep	190	200	210	220	230	
	AAKLTQQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESD	TDXX				
m792	190	200	210	220	230	
	AAKLTQQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESD	TDXX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2687>:

g793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTTGT TTTGAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACAC CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGC^ATAT
651 TTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTGCTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCA. GTCCG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGCGGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAAACCGGC
1501 ACGGCGCGCA AGTTCGTCAA CCGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCTGTGT ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCGCAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YDGGAEVVL RDRQGNIVDS LDSRPNKAPQ NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEM YDFYHELIG VMHSGFPGE
401 TAGLLRNWRR WRPIEOATMS FGYGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGAKTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGGVVVA
551 GPPFKIMGG SLNILGISPT KPLTAAAVKT PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTTGT TTTGAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACAC CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGCAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGTTTCG GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTGGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGGTGGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCCGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRIST MAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVFK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRRG RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLO LARAYTALTH DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYVGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFKLEQ					
m793	MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFKLEQ					
	10	20	30	40	50	60
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVFKDMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVFKDMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
g793.pep	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
	190	200	210	220	230	240
g793.pep	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRRGRADSEQRRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRRGRADSEQRRNR					
	250	260	270	280	290	300
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYKIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYKIGPSPVRDTHVYPSLDVRGIM					
	310	320	330	340	350	360
g793.pep	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMS					
	360	370	380	390	400	410

1276

	430	440	450	460	470	480
g793 . pep	FGYGLQLSLLQLARAYTAL	THDGVLLPLSFEKQAVAPOG	KRIFKESTAREVRNLMVSVTE			
m793	FGYGLQLSLLQLARAYTAL	THDGVLLPLSFEKQAVAPOG	KRIFKESTAREVRNLMVSVTE			
	420	430	440	450	460	470
	490	500	510	520	530	540
g793 . pep	PGGTGTAGAVDGF	DVGAKTG	TARKFVN	GRYADNKHVAT	FIGFAPAKNPRVIVAVT	IDEPT
m793	PGGTGTAGAVDGF	DVGAKTG	TARKFVN	GRYADNKHVAT	FIGFAPAKNPRVIVAVT	IDEPT
	480	490	500	510	520	530
	550	560	570	580		
g793 . pep	AHGYYG	GGVVAGPP	FKKIMG	SLNILGISPTKPLTAAAVKTPSX		
m793	AHGYYG	GGVVAGPP	FKKIMG	SLNILGISPTKPLTAAAVKTPSX		
	540	550	560	570	580	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

a793 . seq

```

1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTACGGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAAC TTGCGGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCATAA
301 GAGATGAAGG AATGCCGTC TGCCGCACAA TTGGAACGCC GTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTTA CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AAT'AAAAAG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGT'TTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 AGCATCATCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TCCGCAAGG CGGTGGAATA CCATCAGGCA AAAGCCGGA CCGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACACGC GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCAGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCG GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGCGCTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAAACG ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGCGCGG TCGGTGGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

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This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

a793 . pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLK QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVSFE
451 EQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLOTVTYNFLKEQ					
m793	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLOTVTYNFLKEQ					
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	130	140	150	160	170	180
	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELGI GVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELGI GVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTDGVLLPVSFQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTDGVLLPVSFQAVAPQGKRIFKESTAREVRNLMVSVTEP					
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVVGAKTGARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	490	500	510	520	530	540
	GGTGTAGAVDGFVVGAKTGARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTTCCTACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCCGCGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTGG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGCGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRFNFHIMVT IIIYVISPAN KPVRPRGPVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHR'
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWALSGG
151 PVFNOENLLA VORQLRDKGI RNITGRMLD HSLWGEVSGP DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLTRNRF KQSGGLLRLE
451 TGTINNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDALMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCGGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTTCAAAC
351 CTTGGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTTGGCGGG CAGCGGCGAC
451 CCGGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCT AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACCTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTGG TCATCATCAA CAGCGGCGCG GCGGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AOKQLREOGI LNTIGHLMLE HSLWGEVGSF DFEADSGSP
201 FMTPPNPTML SAGVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLK LRGNIPECL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFMVTIIIIYVISPANKPVRRPGVPTYPALPYNCFFYVTDSPMNFPKTAASLLLLL					
m794	VRLNHFMIAIIIIYVISPANKPARRHSVPTYPALPYNCFFYVTDLPNMNFPKTAASLLLLL					
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS					
m794	ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
	70	80	90	100	110	120
g794.pep	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQKQLRLKGI RNITGRMLLD					
m794	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREOGI LNTIGHLMLE					
	130	140	150	160	170	180
g794.pep	HSLWGEVGSFDDFEADSGSPFMTPPNPTMLSAGVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGSFDDFEADSGSPFMTPPNPTMLSAGVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKL RGNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKL RGNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTP EGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTP EGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRRELAVSGIDVADLVL ENGSGLSRKE RVTARMAQMLETAYFSPFA					
m794	GKLPVSEQAASAVRRELAVSGIDVADLVL ENGSGLSRKE RVTARMAQMLETAYFSPFA					
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDGT LRNRFKQSGGLRLK TGTLLNVRALAGYWLGDKPM AVVVIINSGR					
m794	QDFIDTLPIAGTDGT LRNRFKQSGGLRLK TGTLLNVRALAGYWLGDKPM AVVVIINSGR					
	430	440	450	460	470	480
g794.pep	AVSLLPDLDNFVAKNIISGGDGWLDKLMCKERRAX					
m794	AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCCAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTG CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTAQC GCGTTTGCCG CCTTCAAAAC
351 CTTGGGACGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCTCCCAA
751 GCTGCCTGCC CTTGCGATCA AAAACTGATG CGTGCACTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACCTGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCAATC
951 CGACACGCGG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAATCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGCGGAC GGCAAACTGC CCGCGGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAACCGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGTAACGG CGAGAATGAT GCGGCAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTCCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTCG AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```

1 VRLNHFIMIA IIIYVISPA KPARRHVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALD GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGS PDFFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDGKPM AVVVIINSGR AVSLPDLN FVANNIISGG
501 DGWLDALMC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIYVISPA	KPARRHVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIYVISPA	KPARRHVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
	10	20	30	40	50	60
	70	80	90	100	110	120
a794.pep	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	ASTMKLVTA
m794	ASLAHALDT	GRIPONEIA	VYVQELDS	GVIIIDHR	SDVPVNP	ASTMKLVTA
	70	80	90	100	110	120
	130	140	150	160	170	180
a794.pep	NYRWATEFK	SNGTVNDG	LDGNLYWA	GSGDPVFN	QENLLAVQ	RQLREQGIR
m794	NYRWATEFK	SNGTVNDG	LDGNLYWA	GSGDPVFN	QENLLAVQ	RQLREQGIR
	130	140	150	160	170	180
	190	200	210	220	230	240
a794.pep	HSLWGEVGS	PDFFEADSG	SPFMTPPN	PTMLSAGM	VVMVRAE	RNAADSTD
m794	HSLWGEVGS	PDFFEADSG	SPFMTPPN	PTMLSAGM	VVMVRAE	RNAAGSTD
	190	200	210	220	230	240
	250	260	270	280	290	300
a794.pep	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKR	GNIPESCL	GKPVGVRM
m794	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKR	GNIPESCL	GKPVGVRM
	250	260	270	280	290	300
	310	320	330	340	350	360
a794.pep	NHWLLGGG	RISDGIGI	SDTPEGAQ	TLAVAH	SKPMKEIL	DMNKRSDN

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```

|||||
m794      NHWLLGGGRISDGIGIADTPEGAQTL...HAKPMKEILTDMNKRSNLIARSVFLKGGD
          310      320      330      340      350      360
          370      380      390      400      410      420
a794.pep  GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMM AQMLETAYFSPFA
          370      380      390      400      410      420
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRF ERVTARMM AQMLETAYFSPFA
          370      380      390      400      410      420
          430      440      450      460      470      480
a794.pep  QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGD KPM AVVV IINSGR
          430      440      450      460      470      480
m794      QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGD KPM AVVV IINSGR
          430      440      450      460      470      480
          490      500      510
a794.pep  AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          490      500      510
m794      AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGC GCGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGCGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAAGTTT TTTCGCCTCG
251 CCCC AAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTTCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcg cATTTCgacg tgttgGATTT GGTGCGGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCGG CATTGGCTTG AACGGCGGCT TGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGTAGAAGG TGGTGCCTC GGGGTCGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTCGCT ATCGGGGTTT TGCGCCGCGC GGACGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgcgCCGA TTATACCGGA TTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FORADADRIA YFIQOFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAF AQFCQ FGVDFRRRK FRLAPSQAVG KHLRKFRFRF
101 RRGEGFIDFK QRA FVGLFRL ARLFHVGNDF VDRFLGFFV FPKRNGIAVG
151 FGHFASVQTD QEFDFVDFH FGQGEFLET VGEAAGNVAR HFDVLDLVAP
201 DGD FVGVEHQ NVGSHQNRIT EQTHFHT EIG VFLPVFRIGL NGGFVGVGAV
251 HQTLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG NGNLGGLVNH
301 LLLVAFDDAV VIGEEBEGFG IGVLRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMP SEREK DAPIIPDLPH TSSRQOTFPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTCTG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG

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1282

```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCACAC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
401 TTGTCTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CCGGCAGGGT GAAGAGTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGT .TGAAG GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFQRA DADRIXFVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRRRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNLRLV
301 AFDDEVVIGE EEEFGGIEVL RRADGGADGA DVVAQMRDAG GGYAQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

          10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRACLQNLFDLRRVGGQ
          |||||  |||||  |  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

          60      70      80      90      100     110
m900.pep  LVVAFARFGEFGVDFFRQKFFGFTPRQAVGKHFRKFHRRRRRGEGFVDFKQWAFVGLFRL
          |||||  |  :|||  |||||  |||||  :||  :||  |||||  |||||  |||||  |||||
g900      CVVAFQAQFCQFGVDFFRRKFFRLAPSQAVGKHLRKFRFRRRRGEGFIDFKQRAVGLFRL
          70      80      90      100     110     120

          120     130     140     150     160     170
m900.pep  ARLFHIIGDDFVDRFLGFFVVFPRKNGVAVGFGHFPASVQTDQEFDFVFIDFHFGQGEFPEA
          |||||  |  :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFPASVQTDQEFDFVFDFHFGQGEFLET
          130     140     150     160     170     180

          180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFIRIGL
          190     200     210     220     230     240

```



```

      240      250      260      270      280      290
m900.pep HGGFVGMGAVHQTLGSDAGQNPNVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      NGGFVGVGAVHQTLGGDAGQNPNVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL
          | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      LLLVAFDDAVVIGEEEEFGIGVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep AASMPSEREKDVPIIPDLPTSSRQQTFFPYX
          :|:|||||:|||||:|||||:|||||
g900      TAAMPSEREKDAPIIPDLPTSSRQQTFFPYX
          370      380      390

```

a900.seq	(partial)					
1	GAGGTTCCGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCCGAT	
51	CACGCTACTTT	GCCCAATAAT	TCGGGTGCTT	CTTTACGGCG	TTTTTGCGCG	
101	CTGCGCTGCA	AAATCTCTTC	GATTTCGGAA	GGGTGCGCGG	TCAGCTCGTT	
151	GTAGCGTTTCG	CGCGGTTCGG	CGAGTTCGGC	GTTGATTTTC	GCGCCCAAAT	
201	GTTTTTTTTCG	CTCGGCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTCGTAAT	
251	TCTGCGGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATT	CAAAACGAGG	
301	GCTTTCGTTCG	GGCTTCTTCG	GCTCGCCCGG	CTCTTTCATA	TTGGTGATGA	
351	TTTTGTGTAC	CGATTTTTTG	GTTTTTTTGT	CGTTTTCCCA	AAGCGGAATG	
401	GTGTTGCCGT	AGGATTTGGA	TTTCTTGCGT	CCGTCCAAAC	CAACCAAGAG	
451	TTTCGACGTTT	TGCTCGATT	TCACTTCGGG	CAGTGTGAAG	AGTTCCCGGA	
501	ATCGGTTGGTT	GAAACGGCCG	GCAATATCCG	GTGCCATTTC	AACGTTGTTG	
551	ATTTGGTTCG	GACCGACTGG	AACTTCATGG	GCATTGAACA	TGAGAATGTC	
601	GGCAGTCATG	AGGATAGGGT	AGCTGTACAA	ACCCATTTCC	ACGCCGAAAT	
651	CGGGGCTCTC	CTGCCCGTTT	TCCGCAATTG	CTGCGACGGC	GGCTTTGTAG	
701	CGGTGGGCGC	GGTTCATCAA	ACCTTATGGC	GTGATGCAGG	TCAGAATCCA	
751	GTTCAATTCC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC	
801	GCTCGGGGTC	GAGTCCGCAG	GCAAGCCAA	TGGCGGCAC	GGCTTTGGGTG	
851	GATTGGTGAA	TCATCTCCGG	CTCGTGGCAT	TTGATGCAT	CGTGGAATC	
901	GGCGAGGAAG	AGCAAGGATT	CGGTATCAGG	GTTTTGCGCC	CGCGGGACGG	
951	CGGGGCGGAT	AGCACCGACG	TAGTTGCCCA	GATGCGGGAT	GCCGGTGGTG	
1001	GTTACGCCGG	TCAGAAATCG	TTTTTTGCTC	ATAAAAAATG	CCTTGGCGGA	
1051	TCAATGCCGT	CTGAAAGGGA	AAAGATGCGC	CCGATTATAC	CCGATTTGCC	
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA		

a900.pep	(partial)				
1	EVRTALGLFQ	RADTDRITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV
51	VAFAERGEFG	VDFRRQKFF	LAPSQAVGKH	FRKFCRFRRR	GESFVDFKQR
101	AVEGLLRLAR	LFHIGDDEVD	RFLGFFVFP	KRNGVAVGFG	HESVQTNQE
151	FDVFVDFHFG	QCEEFPAAV	EAAGNIACHF	NVLDLVATDW	NFMGIEHENV
201	GSHEDRVAVQ	THFHAIGVF	LPVFRICLHG	GFGVGAVHQ	TLGGDAGQNP
251	VQFHHFGNVA	LVTEGGALGV	ESAGKPSGGN	GLGLVNHILR	LVAFDDTVVI
301	EEEEEGFGR	LTRRDGGAD	STDVVAQMRD	AGGGYAGQNS	FFAHKNVLAA
351	SMPSEKEDA	PIIPDLPTS	SRQTFPY*		

```

      10      20      30      40      50      60
m900.pép  MPSETRQAEVRTASGSFQRADADRIXVFVQXFACFFTRFRRACLQNLFDLRRVGGQLVVA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a900      EVRTALGLFQRADTDRIYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA
          10      20      30      40      50

          70      80      90      100     110     120

```

1284

```

m900.pep    FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRLARLF
|||||
a900        FARFGEFGVDFRRQKFFCLAPSAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRLARLF
          60      70      80      90      100     110

          130      140      150      160      170     180
m900.pep    HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTDQEFDFVDFHFGQGEFFPEAVVEA
|||||
a900        HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTNQEFDFVDFHFGQCEFFPEAVVEA
          120     130     140     150     160     170

          190      200      210      220      230     240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVHEHQNIGSHQNRITEQTHFHEIRVFLPVFCICLHGGF
|||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
          180     190     200     210     220     230

          250      260      270      280      290     300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
|||||
a900        VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
          240     250     260     270     280     290

          310      320      330      340      350     360
m900.pep    AFDDTVVIGEEEEFGFIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVLAASM
|||||
a900        AFDDTVVIGEEEEFGFIRVLRRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          300     310     320     330     340     350

          370      380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFPYX
|||||
a900        PSEREKDAPIIPDLPTSSRQQTFPYX
          360      370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTAKGyAG TGGCTTGGTG ATGTTTTCCT
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATT CCCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCG CT3CCGTGTT
651 TGGTTCGTA TTCCGGCGTA TAGCCGGTGT GATGGTGT TTTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAACGGGTAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

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1285

```

101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
251 YGLTTGMAVI AVSLVLFHF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

```

a901.seq
  1 ATGCCCGATT TTTCGATGTC CAATTGGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTGGCATT TGCCGGCGGT
151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTGGCGCG GCGACCATGG
251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTT AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGCTT GCGATTACTG
401 CGCACAAATT CCCCAGAGGC TTGGCGACGT TTTTGGCAC ATGGGAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTGGCCACC CGCAGCCGTA
551 AGAAAACGCT GTGGCGGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGGTTCGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTTGGCGTTG
701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAACCGTT
751 TACGGCCTGA CAATGGGCAT GCGCGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

```

a901.pep
  1 MPDFMSNLA VAFSITLAAG LETVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
251 YGLTMGMAVI AVSLVLFHF*

```

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLA VAFSITLAAG LETVLXSGLMFMSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	MPDFMSNLA VAFSITLAAG LETVLGSGLMFMSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLVPNPHETLDAQDPSFQESKRRH					
a901	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLVPNPHETLDAQDPSFQESKRRH					
	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLENPAVGMPLALAIAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
	RSRKKTVWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELXPAA					
a901	RSRKKTVWACLLSGLAEPLGAALGYLVLPFLSPAVFGSVFGVIAGVMVFLALDELLPAA					
	190	200	210	220	230	240
m901.pep	250	260	270			
	KRYSDGHETVYGLTTGMAVI AVSLVLFHFX					
a901	KRYSDGHETVYGLTMGMAVI AVSLVLFHFX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```
g902.seq
1  ATGCCGTC CG AACC CGAACG GCGGCATGGC AATACTGCCC TACCCCTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCCGCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGGCGTG GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGCGCTCTG CATCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGCCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGCGGCG TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTGGT CTGGGcgatg agttCGTAAC
501 gcGCTCGCC TTTGTACATT TGCGTGcgcG CGcgcccg tg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcg gcaggttttg
601 atcgtcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTcttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcg
801 catCCGCCAT CtggttcggGG TCGCTGCCGG CAATCTGCAC tttAACGATC
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGCGGCGG AAGGGTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```
g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGAADVQN GGSAPCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAlF GDFDGGQVL
201 IVVVPQTGF EGNVYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```
m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT T GGC CGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGTTGA TTTACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGTTTCA AAATAGCGGC GCGCATCTCT GCCAAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGTTTTCGGC GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCCT
851 TCATCGCAA AATCGCTGCG GTGCAAGGT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1287

```

m902.pep
1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQGRR
101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS	EGIWAVGARPTV	GFFGKSFKIT	CKHVVLRRRT	VQAVDFTTCL
		:	:	:	:
g902	10	20	30	40	50
	MPSEPERRHGNTAL	PFPIAARPTV	GFGSGKPFKIT	GKCVVLRRRI	VQAVDFTPRL
		:	:	:	:
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHT	GGVAVKRVYG	ADVQNSGGAFC	QQTQGRRQNT	VFGIMFQIAE
	:	:	:	:	:
g902	60	70	80	90	100
	ADVPAVFACDAHTD	GLTIKRVHGAD	VVQNGGSAFC	QQTQGRRXNA	VFGIMLQIAE
		:	:	:	:
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGL	FEDGLGFLRR	SNVAVDPD	DRDVTAFGFG	DEFVTRFAFV
	:	:	:	:	:
g902	120	130	140	150	160
	LRAAPYHNAVGGGL	FEDGGGFLRR	SDVAVD	PGRDVTAFGL	GDEFVTRLAF
		:	:	:	:
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFG	DDGQVLMVV	PTQTGFEGNG	YACRTDDG	FQNGGNQRLV
	:	:	:	:	:
g902	180	190	200	210	220
	NGKGGNAIFGDFG	DDGQVLIVV	PTQTGFEGNG	YARRLDHRL	QNGGNQRLV
		:	:	:	:
m902.pep	240	250	260	270	280
	DIADFFSGTAHV	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA
	:	:	:	:	:
g902	240	250	260	270	280
	DVAHFLGGAHID	VDDLRPESD	VVTRRIRHL	FGVAAGNLH	GNDAAFIGKI
		:	:	:	:
m902.pep	300	310	320	330	340
	ERRVAGQHFAHR	PTCAKISAKS	AERFVGNARH	RRCDCGVVDK	IAADVHNGSA
	:	:	:	:	:
g902	300	310	320	330	340
	ERRIAGQHFAHR	PTCAKRPTAA	EGFVGNARH	RRCDCGVVDK	ITADVHNGSA
		:	:	:	:
m902.pep	360				
	IFX				
	:				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTG GGCCTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAGG ATAACCTGCA

```

1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAAACACCG TGTTGCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCGCT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTGCGTG CGCGTCGCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTGAGGGT AACGGGTACG CCCGCGCCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACCC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```

a902.pep
1 LHFQRIIKCS EGIWAVGARPTVGGFFGKSFK ITCKHVVLRRTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRSAIR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPP
151 RDVQTAFGFG NQVVSRRFAFV HLRARASVDG KGGNAAI FGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSCTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FOKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

```

          10      20      30      40      50      60
m902.pep  LHFQRIIKCSEGIWAVGARPTVGGFFGKSFKITCKHVVLRRTVQAVDFTTCLFAVGHFVD
          |||
a902       LHFQRIIKCSEGIWAVGARPTVGGFFGKSFKITCKHVVLRRTVQAVDFTTCLFAVGHFVD
          10      20      30      40      50      60

          70      80      90      100     110     120
m902.pep  VPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQQTQGRRQNTVFGIMFQIAEEPRPALR
          |||
a902       VPAYVFACDAHTGGVAVKRVHGSDDVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRSAIR
          70      80      90      100     110     120

          130     140     150     160     170     180
m902.pep  AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFFGFGDEFVTRFAFVHLRTRASVDG
          |||
a902       AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFFGFGNQVVSRRFAFVHLRARASVDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m902.pep  KGGDAAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLV LHQRATGLDI
          |||
a902       KGGNAAI FGD FGD GQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLV LHQRATGLDI
          190     200     210     220     230     240

          250     260     270     280     290     300
m902.pep  ADFFSCTAHVDVDKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
          |||
a902       ADFFSCTAHVDVDKLRPKADVTRGIK...LRIASGNLHGNNAAFIGKIAAVQGFSSISER
          250     260     270     280     290     300

          310     320     330     340     350     360
m902.pep  RVAGQHFHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF

```

1289

```

|||||
a902      RVAGQHFAHRPTCAKISAASAEERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTFLYIF
              310      320      330      340      350      360

m902.pep      X
                |
a902          X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51  TCCTATTCTT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTCcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCGGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGA ACAAGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtagAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGTAAC GTCTGTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAAATTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCTTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCGCTA ACATCGCAAG ACAAAGTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatattt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDLEQL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYGK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFLKL
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLAD VGHVSGQSAK WLSGQTLAQT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWTGFG VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAAATGT
51  CCGTTTCGAG CAACCATTGG AGAAGAACAA TTATGCTCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

```

151 CGCAAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TCGCTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAAT TACAGCGTGC ATTATTGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAACTTCA GTCCGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTTCAGC TTGACGGCAA
1101 GTTGCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCAGGTA CATCTCGTAT GAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AYTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

```

m903.pep
1  MQRQQHIDAE LLTDANVRFE QPLEKNNVVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTGM CLGSNNLSRL QKAAQILIV RGYLTSQAI I
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFLYRNNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQQNKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLA AERM LWRNRLH KTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRH RAYLN RWQLDGKLSY KRGTM RQSM PAPEENG GDI LPGTSRMKII
401 TASLD AAA PF XLGKQ QFFYA TAIQA QWNKT PLVAQ DKLSI GSRYTVRGFD
451 GEQSL FGERG FYWQNTLTWY FHPNH QFYLG ADYGR VSGES AQYVSGKQLM
501 GAVVG FRGGH KVGGM FAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNVVLSEDETPCTRV NYISLDDKTVRKFSFLPSVL
                                     |:::||| :::| :::| | :
g903      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
                                     10      20      30

          70      80      90      100     110     120
m903.pep  MKETAFKTGMCLGSNNLSRLQKAAQILIVRGYLTSAIIQPQNMDSGILKLRVSAGEIG
          : :| | :| || ::::: : ||: || ||| |::: | |::| | :| :| :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLTLMPGYLR
          40      50      60      70      80      90

```


1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQIIPSE					
g903	SIRIDRSNDDQTHAGRIAAFQNKFPTRSNLLNLRDLEQGLNLRCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQONK-PIRFSIGIDTAGGKTTGKYQGNVALSFDNPLGLSDFYVSYGR					
g903	REPNSQSDVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMPYVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTDATGTETESGSRYSVHYSPVKKWLFSPNHNHRYHEATEGYSVNYDYG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNHRYHQAVSGLEVDYDYG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSMGKMLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRTKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAPFXLGKQOFF					
g903	IGRSTADFKLKYKHGTGMKDALARPEEAFGE---GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAWNKTPPLVAQDKLSIGSRYTTRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPPLTSQDKLAIGGHHTVRGFDGEMSLPAERGWWYWRNLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFGRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGRQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
g903	TGFOVGYSFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

```

1   ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATGG  AGAAGAACA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA  AATTACATTA GTTTAGATGA TAAGACGGCG
151 CGCAAATTTT CTTTCTTCC  TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT  CCAATAATTT GAGCAGGCTA CAAAAGCCG
251 CGCAACAGAT ACTGATTGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAACCACAGA ATATGGATTC GGAATTCTG  AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCGGA  GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT

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1292

```

601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTC AAT AC GATTACAA CCGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGCGGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT C AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGFSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ
301 YQSSLAER M LWRNRFHKT S VGMKLWTRQ T YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMQRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTXXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL G ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTA	VRKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTA	VRKFSFLPSVL
	10	20	30	40	50	60
m903.pep	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAII	QPQNMDSGIL	KLRVSAGEIG
	70	80	90	100	110	120
m903.pep	DIRYEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQIIPSE
a903	DIRYEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQIIPSE
	130	140	150	160	170	180
m903.pep	EEGKSDLQI	KWQONKPIR	FSIGIDDAGG	KTTGKYQGN	VALSFDNPL	GLGLSDFYV
a903	EEGKSDLQI	KWQONKPIR	FSIGIDDAGG	KTTGKYQGN	VALSFDNPL	GLGLSDFYV
	190	200	210	220	230	240
m903.pep	AHKTDLTDA	TGTETESG	SRSSVHYS	VPVKKWL	FSFNHNGH	RYHEATEGY
a903	AHKTDLTDA	TGTETESG	SRSSVHYS	VPVKKWL	FSFNHNGH	RYHEATEGY
	250	260	270	280	290	300
m903.pep	SVNYDYNGK	Q				
a903	SVNYDYNGK	Q				

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEPEENGDDILPGTSRMKIIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEPEENGDDILPGTSRMKIIITAGLDAAAPFXLGKQQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

```

g904.seq
1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCCGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTCGTTCAA CACGCGggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGCT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGTAAGG CAGGATCAGC GGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGTCGGA ATCAGGCGCA AAATGGTTTT TTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

```

g904.pep
1  MMQHNRFFAV GAGGDDGDRR AADFFNPFI CFGRQCVV AFHADSRFAP

```

1294

```

51 AGHGFVNRF A GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDV IGKDG IQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFARCF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYNYIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904 . seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATAACGGAA ATGCCGTTGA TTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CGGTGCGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCGGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCG. ACT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGAC ACCTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTyTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCTG
901 GCCGATTTTG CTTTGGCCGC GCG. ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCAcGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904 . pep
1 MMQHNRRFFSV GAGGDDGDRR AADFFNPFOI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRLA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXNYIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904 . pep MMQHNRRFFSVGAGGDDGDRRAADFFNPFOICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
g904 MMQHNRRFFAVGAGGDDGDRRAADFFNPFOICFGIGRQCVVAFHADSRFAPAGHGFVNRF
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGFAAVGFQFIADADIDGFNAVHYIEFSNTHGTGNAVLDGAFQGGGIKPA
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVSAPCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGHNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQORTLRAFQKQFFAVFVFFVQHAGHVGHNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQIQGGANGAACHFV FVGRADAAAGR
g904	HHVFRFNRS GVMQVLELDV VIGKDGIOFFTQFFRMQIQGGANGAACHFV FVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADF AFAARI FAGLVERDVVRQDQRAGR RDFQTAFDV FHACRVQLVDF AQGGFGGDDNART
g904	ADF AFAARC FAGLVERDVVRQDQRAGR RDFQTAFDV FHACRVQLVDF AQGGFGGNDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVA ALEAHHAAGFFRQFPVNDFTFTLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADNQGMARIVA ALEAHDAAGFFRQFPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATAACCGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCCGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTGC TCCGACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGGCCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTTGCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGCT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC TCGGGCTTGG TCGAGCGCGA

```

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACG GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

```

a904.pep
1  MMQHNRRFAV GAGGDDGDRR TADFFNPFQI CFGICF*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRAA*Q DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKP* AAACASGYRT EFVS AFCQ* C SDFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDG IQFFT QFFRMQQIGG ANGAACHEVF VGRADAAAGR
301 ADFAFARCF SGLVERDVIR QDQRAGRRDF QTAFDV FHAC RVQLVDFAQQ
351 GFGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYNI FSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVVAFHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFAAVGFQFIADADIDGFNAVHYIEFSNTHTCNAVDLDGAFQGGGIKPA					
a904	GFYRIRAAQDVGFAAVGFQFVADADIDGFNAVHYIEFGNTHTCNAVDLDGAFQGGGIKPA					
	70	80	90	100	110	120
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRYARACRS					
a904	AAACASGYRTEFVS AFCQTCSD FVEQFGRERARTDARGIGFDDAQNI IQHLRAYARACRS					
	130	140	150	160	170	180
m904.pep	190	200	210	220	230	240
	CARQTVGRNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR					
a904	RAGEAVGRSNEGVSA VVDVQORTLRAFQKQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTQFXRMQQIGGANGAACHEFVFGVGRADAAAGR					
a904	HHVFRFHRLGIVQMLQLDVVISKDG IQFFTQFFRMQQIGGANGAACHEFVFGVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDV FHACRVQLVDFAQQGGGDDNART					
a904	ADFAFAARCFSGLVERDVIRQDQRAGRRDFQTAFDV FHACRVQLVDFAQQGGGDDNART					
	310	320	330	340	350	360
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQGMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

```

g906.seq      not found yet
g906.pep      not found yet

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGA AAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACTTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFEG FKPWPDAAS FWELKNYANP YPGSASAALD
51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGCTt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTCGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGCCA AGATTCGTCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51 GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGCCA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTAT GCCGTTkTGG AAAAActACA TCGGCAAAAC GGCGCACAAAC
451 CTGTTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGCGG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYASGVGA RGLMQVMPXW XNYIGKPAHN

```

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151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCCT
51  ATTGTGTGCT GCCGCGCGCG TGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTGCGCA GCATAAATCC GCCGAGGCTG GTGTTTCGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCTGTC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTAT GCCGTTTTGG AAAAATACTA TCGGCAAACC GGCGCACAAC
451 CTGTTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQR EETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAIISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARENGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQR	EETLADDVASVMR	SSVGSVNP	PRL		
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQR	EETLADDVASVMR	SSVGSINP	PRL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAI	SGVG	ARGLM	QVMP	KWNY	IGKPAH
a907	RQYAI	SGVG	ARGLM	QVMP	KWNY	IGKPAH
	130	140	150	160	170	180
	190	200				
m907.pep	ARENG	SLGS	SNKYP	NAVL	GAWR	NRWQWRX
a907	ARENG	SLGS	SNKYP	NAVL	GAWR	NRWQWRX
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMPD GEVEADESYF GGQRKGKGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYDCY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAAC
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAC CCTGACAGCA TTTTATATAC GCATTGTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMPD GEVEADESYF GGQRKGKGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYDCY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng)

from *N. gonorrhoeae*:

	10	20	30	40	50	60
g908/m908						
g908.pep	MXKSRLSRYK	QNKLIGLFV	AGVTARTAAEL	VGINKNTAAY	DFHRLRLLIY	QNGPHLEMPD

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m908	MRKSRLSQYKQXKLIELFVTGVGTARTAAELVGVNKNTAAAYYFHRLLLIYQNSPHLEMF
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNKGKVVTVTPNTQTATLFPIIREQVK
	70 80 90 100 110 120
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNKGKVVTVTPNTQTATLFPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTD CYRSYDVLVDVSEFHSFSAETSF SYQS QHTFCRTTKPYX
	130 140 150 160
m908	PDSIFYTD CYRSYDVLVDVREFSHFSAETSF SYQS QHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

```
a908.seq
1  ATGAGAAAAA  GTCGTCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTCGCA  GGTGTAAC TG  CAGAACGGC  AGCAGAGTTA  CTAGGCGTTA
101 ATAAAAAATAC  CGCAGCCAT  TATTTTCATC  GTTTACGATT  ACTTATTTTA
151 CAAAACAGTC  CGCATTGGA  AATGTTTGAT  GCGCAAGTAG  AAGCAGATGA
201 AAGTTATTTT  GCGGGAACA  GCAAAGGCAA  ACGCGGTCGC  GGTGTCGCCG
251 GTAAAGTCGC  CGATATTCGT  CTTTTGAAGC  GAAATGGTAA  GGGTTATACG
301 GTTACAGTAC  CGAATACTCA  AACCGCTACT  TTATTTCCCTA  TTATCCGTGA
351 ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATTGTTAT  CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA  TTAGCCATT  TTAGCTTCGC  TGAAACTTCG
451 TTTTCGTATC  AATCAGACGA  CACATTTTGC  CGAACGACAA  AACCATATTA
501 A
```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

```
a908.pep
1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNTAAY YFHLRLLIY
51  QNSPHLEMFQ GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNKGVYT
101 VTPVNTQTAT LFPPIREQVK PDSIVYTCY RSYDVLQVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*
```

m908/a908 98.2% identity in 166 aa overlap

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAAYFHRRLLLIYQNSPHLEMFD					
a908	MRKSRLSQYKQXKLIELFVAGVTARTAAELVGVNKNTAAAYFHRRLLLIYQNSPHLEMFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPTQTATLFPIIREQVK					
a908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPTQTATLFPIIREQVK					
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFYSYQSQHTFCRRTTKPYX					
a908	PDSIVYTDCYRSYDVLDVREFSHFSFAETSFYSYQSQHTFCRRTTKPYX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```
g909.seq (partial)
      1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc ttttgtcggg
     51  ctgcacatgG gaaacttatac aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg
```

1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtggtgag
201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggagagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CTGACCGCT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR			
g909	ERRAVLRNQR	KGKPTRRAAT	LGKPSFRAR	DGGGRVNRAE	TGEKRSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CTGATGACT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILILMT AAALLSGCAW ETYQDGNgKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
a909	MRKTFILILMT	AAALLSGCAW	ETYQDGNgKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

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	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEE	HRQHWQPKFQNRX
a909	ERHAVLPNQ	TGNNADEE	HRQHWQPKFQNRX
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910.pep	MKKLLLAADV	SLNAATAFAG	DSAERQIYGD	PHFEQNRTKA	VKM	LEQRGYQVYD
m910	MKKLLLAADV	SLSAAAFAG	DSAERQIYGD	PHFEQNRTKA	VKM	LEQRGYQVYD
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAY	KDGREYDIVL	SYPDLKIIKE	QLDRX		
m910	GKPVLEVEAY	KDGREYDIVL	SYPDLKIIKE	QLDRX		
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

```

1  MKKLLLAVVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

m910/a910 95.7% identity in 94 aa overlap

```

              10      20      30      40      50      60
m910.pep      MKKLLLAAVVVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVVDVDADDHW
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910           MKKLLLAVVVSLSATAFAGDSAERQIYGDPIYFEQNRTKAVKMLEQRGYQVHDVDADDHW
              10      20      30      40      50      60

              70      80      90
m910.pep      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910           GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

```

g911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATTT GGACGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

```

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

```

g911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

```

m911.seq
1  ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

```

m911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng)

from *N. gonorrhoeae*:

g911/m911

```

              10      20      30      40      50      60

```

1304

```

g911.pep      MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              |||||
m911          MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              |||||
m911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              |||||
m911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51  CGCGCGCGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGCGCT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAC CTTATCGGCA AATTATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep      MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              |||||
a911          MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              |||||
a911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              |||||
a911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTGTACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

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```

151 CGCCCAAAAG CCGAAGCCTA TCGGTTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGCGGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATAC GTACCTACAA CGTCGCCAT GAAGGCACGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRONATQVLT ILKSGDAASA
51  RPKAEAYAVP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKFNAT VNVKDNPIVN KKGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
1  ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGCGATGC CAACCCGCT
151 CGCCCAAAAG CCGAAGCCTA TCGGATTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
1  MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRONATQVLS ILKNGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLNAN VNVKDNPIVN KKGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912
          10      20      30      40      50      60
g912.pep  VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912       MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

          70      80      90      100     110     120
g912.pep  YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFNATVNVKDNPIVN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912       YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLNANVNVKDNPIVN
          70      80      90      100     110     120

          130     140     150     160     170     180
g912.pep  KKGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTYRNQFGEI IKAK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m912       KKGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
          130     140     150     160     170     180

          190
g912.pep  GIDGLIAELKAKNGGKX

```

1306

```

      |||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1  ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGGCGA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCGGGGCA AAAACCGGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATATCC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1  MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPSQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYVR NQFGEI IKAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

      10      20      30      40      50      60
m912.pep  MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP
      10      20      30      40      50      60

      70      80      90      100     110     120
m912.pep  YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
      70      80      90      100     110     120

      130     140     150     160     170     180
m912.pep  KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYVRNQFGEI IKAK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYVRNQFGEI IKAK
      130     140     150     160     170     180

      190
m912.pep  GVDGLIAELKAKNGGKX
      |||||:|||||:|||||:|||||:|||||
a912      GVDGLIAELKAKNGSKX
      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1  atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAAGTTT GGCAGCAATA
251 TCTTGCGTTT GGAcatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGcgcGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgctccac

```


g913.pap

m913.seq

m913.pcp

q913/m913

	10	20	30	40	50	60
g913.pep	MKKTAYAILLLIGFASAPAF	AETRPADPYEGYNRAVSK	FNDQADRYIFAPAARGYR	KVTP		
m913	MKKTAYAFLLLIGFASAPAF	AETRPADPYEGYNRAVF	KFNDQADRYIFAPAARGYR	KVAP		
	10	20	30	40	50	60
	70	80	90	100	110	120
g913.pep	KPVRAGVSNNFNLRDVVS	FGSNILRLDIKRASEDL	VRVGINTTFGLGGLIDI	AGAGGVP		
m913	KPVRAGVSNNFNLCDDVS	FGSNILRLDIKRASEDL	VRVGINTTFGLGGLIDI	AGAGGP		
	70	80	90	100	110	120

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	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYPPKNIVFHT	PAGRWGTT			
m913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRT	PVGRWGTT			
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCGCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAAGCTT GGCAGCAATA
251 TCTTGCGCTT AGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCCACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC CGCGGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCGGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVEKEN DQADRYIFAP
51  AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPLVGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AADKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVEKEN	DQADRYIFAP	AARGYRKVAP
a913	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVEKEN	DQADRYIFAP	AARGYRKVAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVRAGVS	NFFNNLCDVVS	FGSNILRLDI	KRASEDLVR	VGINTTFGL	GGLIDIAGAGGIP
a913	KPVVRAGVS	NFFNNLCDVVS	FGSNILRLDI	KRASEDLVR	VGINTTFGL	GGLIDIAGAGGIP
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTF	ASWGWKNSNY	FVLPLVGPST	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT
a913	DNKNTLGDTF	ASWGWKNSNY	FVLPLVGPST	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgcttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTC TGCCGATTCTG
451 taggcttCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCG
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLW
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGA GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTGACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTGTTG
601 CTGGTGTGCG CGTAATGAC GGCTTTCGCG CCGAAGCCGA TGCGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng)
 from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCCKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCCKFDXCIGWTDKETDTD					
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCCKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCCKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTRGCRTTSSPVKVKYSPATP					
m914	TELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTRGCRTTSSPVKVKYSPATP					
m914	TELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
	130	140	150	160	170	180
g914.pep	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIF ICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIF ICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
g914.pep	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIF ICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIF ICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCGC	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCCGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTCGCA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCTGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTC	TGCCGATTCG
451	TAGGCTTCGA	CGATTTTGTG	CACCAAAGGA	TGCCGGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCATTGTT	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCTGCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMPAFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCDEA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LECQSCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPN D	MFLGRSIWLV
201	SPVMTAFAPK	PMVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

m914/a914 98.4% identity in 244 aa overlap

```

      10      20      30      40      50      60
m914.pep  MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC
          |||
a914      MKKCILGILTACAAMPADFADRIDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m914.pep  SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD
          |||
a914      SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--
      70      80      90     100     110

      130     140     150     160     170     180
m914.pep  TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSSPVKVWYSPSTL
          |||
a914      TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSSPVKVWYSPSTP
      120     130     140     150     160     170

      190     200     210     220     230     240
m914.pep  CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
          |||
a914      CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
      180     190     200     210     220     230

m914.pep  LPRIX
          ||||
a914      LPRIX
      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

```

g915.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gTtTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

```

g915.pep
1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

```

m915.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

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451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```

m915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```

m915/g915
      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
g915      MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
      10      20      30      40      50      60
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
g915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
g915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
      70      80      90     100     110     120
m915.pep GFIGGGAEDALPFGNKEQA EKFAKDGGKVVVGFDMPDTYIFKX
          |||||
g915      GFIGGGAEDALPFGNKEQA EKFAKDGGKVVVGFDMPDAYIFKX
          |||||
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```

a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCCG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTGCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```

a915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

```

      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
a915      MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||
      10      20      30      40      50      60
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
a915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS
          |||||
      70      80      90     100     110     120

```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIFGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX					
a915	GFIFGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc t3cttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACATAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGGACACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGACAG
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

```
m917.pep
1  MTKHLPLAVL  TALLLAACGG  SDKPPAEKPA  PAENQNVLK  YNWSEYVDPE
51  TVADFEKNG  IKVTYDVYDS  DETLESKLP  KSGYDIVAP  SNAFVGRQIK
101 AGAYQKIDKS  LIPNYKHLNP  EMMRLLMDGD  PGHEYAVPFY  WGTNTFAINT
151 ERVKKALGTD  KLPDNQWDLV  FDPEYTSKLK  QCGISYLSA  AEIYPMVLNY
201 LGKNPNSSNT  EDIREATALL  KKNRPNIKRF  TSSGFIDDLA  RGDTCVTIGF
251 GGDNLIAKRR  AEEAGGKEKI  RVMPKPEGVG  IWVDSFVIPK  DAKNVANAHK
301 YINFLLDPEV  SAKNGNFVTY  APSSKPAREL  MEDEFKNDNT  IFTTEEDLKN
351 SFIMVPIQPA  ALKFMVRQWQ  DVKAGK*
```

m917/g917

370

1315

```

m917.pep    ALKFMVRQWQDVKAGKX
            |||||
g917        ALKFMVRQWQDVKAGKX
            370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

```

a917.seq
1  ATGACCAAAC ATCTGCCCTT GCGCGTCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAATTT TACAACCTGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCTGT
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATCCCA ATTATAAACCA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GCTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTGCGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATCGCGGA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCGAAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAGA GGGCGTGGG ATTTGGGTGG
851 ATTCTTTCGT GATCCGAAA GATGCGAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCACTGGCAG GATGTGAAG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

```

a917.pep
1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDEEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917    99.7% identity in 376 aa overlap

          10      20      30      40      50      60
m917.pep    MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNQ
            |||||
a917        MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m917.pep    IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
            |||||
a917        IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
          70      80      90      100     110     120

          130     140     150     160     170     180
m917.pep    EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLG
            |||||
a917        EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDNQWDLVFDPEYTSKLG
          130     140     150     160     170     180

          190     200     210     220     230     240
m917.pep    QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
            |||||

```

1316

```

a917      QCGISYLDAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRETSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKPEGVGIWVDSFVI PKDAKNVANAHK
           |||||
a917      RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKPEGVGIWVDSFVI PKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNEFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||
a917      YINDFLDPEVSAKNGNEFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKY
           |||||
a917      ALKFMVRQWQDVKAGKY
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAGca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 Caggtagcgt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTGTGTCGCA
551 TCAGGCAGac ggGGAANAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcg tgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAACCCcg tccggcaaat acatCCGCat cggatagcgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcata aaagcCTATA TCGGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTGGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGCGGAAC
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCCAAC
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTGTGVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2791>:

```

m919.seq
1  ATGAAAAAAT  ACCTATTCCG  CGCGCGCCGTG  TACGGCATCG  CCGCGCCCAT
51  CCTCGCCGCG  TGCCAAAGCA  AGAGCATCCA  AACCTTTCGG  CAACCCGACA
101 CACTCCGTGT  CAACGGCCCG  GACCGGCCGG  TCGGCATCCC  CGACCCCGCC
151 GGAACGACGG  TCGCGGCGGG  CGGGGCCGTG  TATACCGTTG  TACCGCACCT
201 GTCCTGCCCC  CACTGGGCGG  CGCAGGATTT  CGCCAAAAGC  CTGCAATCCT
251 TCCGCCTCGG  CTGCGCCAAT  TTGAAAAACC  GCCAAGGCTG  CAGGAGTGTG
301 TGCGCCCAAG  CTTTCAAAC  CCGCTCCAT  TCCTTTCAGG  GCAAACAGTT
351 TTTTGAACGC  TATTTACAGC  CGTGGCAGGT  TGCAGGCAAC  GGAAGCCTTG
401 CCGGTACGGT  TACCGGCTAT  TACGAACCGG  TGCTGAAGGG  CGACGACAGG
451 CGGACGGCAC  AAGCCCGCTT  CCCGATTTAC  GGTATTTCCG  ACGATTTTAT
501 CTCGCTCCCC  CTGCCTGCCG  GTTTCGGAG  CGGAAAAGCC  CTGTGCCGCA
551 TCAGGCAGAG  GGGAAAAAAC  ATTGGCACA  TCGACAATAC  CTTGGCCACA
601 CATAACGCGC  ACCTCTCCcG  ATTCCCATC  ACCGCGCGCA  CAACAGCAAT
651 CAAAGGCAGG  TTTGAAGGAA  GCGGCTTCT  CCCCTACCAC  ACGGCGAACC
701 AAATCAACGG  CGGCGCGCTT  GACGGCAAAG  CCCCGATACT  CGGTTACGCG
751 GAAGACCTGT  TCGAACTTTT  TTTTATGCAT  ATCCAAGGCT  CGGGCCGTCT
801 GAAAAACCCG  TCCGGAAGAT  ACATCCGCAT  CGCCTATTGC  GACAAAACAG
851 AACATCCyTA  CGTTTCCATC  GGACGTATA  TGGCGGATAA  GGGCTACCTC
901 AAACCTCGAC  AAACCTCCAT  GCAGGGCATT  AAGTCTTATA  TGCGGCAAAA
951 TCCGCAACGC  CTCGCCGAAG  TTTTGGGTCA  AAACCCAGC  TATATCTTTT
1001 TCCGCGAGCT  TGCCGGGAAG  AGCAATTGAC  GCCCTGTGCG  CGCATCTGGG
1051 ACGCCCGCTGA  TGGGGGAATA  TGCCCGGACA  GTCAGACCGC  ACTACATTAC
1101 CTTGGGTGCG  CCCTTATTTG  TCGCCACCGC  CCATCCGGTT  ACCCGCAAAG
1151 CCCTCAACCG  CCGATTATG  GCGCAGGATA  CCGGCAGCGC  GATTAAAGGC
1201 GCGGTGCGCG  TGGATTATTT  TTGGGGATAC  GGCAGCAGAG  CCGGCGAAGT
1251 TGCCGCGAAA  CAGAAAACCA  CGGGATATTGT  CTGGCAGCTC  CTACCCAACT
GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

m919.pep

1	<u>MKKYL</u> FRAAL	<u>YGIAAA</u> ILAA	CQSKSIQTFP	QPDTSVINGP	DRPVGIPDPA
51	GTTVGGGGAV	YTVVPHLSL	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAFQTPVH	SFQAQVFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDDR
151	RTAQARFPIY	GIPDDFISVP	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQSGSRLKTP	SGKYIRIGYA	DKNEHPYYSI	GRYMADKGYL
301	KLGQTSMQGI	KSVMRQNPQR	LAEVLGQNPS	YIFFRELAGS	NDGDPVGGALG
351	TPLMGEYAGA	VDRHYITLGA	PLFVATAHPV	TRKALNRLLM	AQDTGSAIKG
401	AVRVDFYFWG	GDEAGELAGK	QKTTGYVWQL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF 'ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

[illegible]

	130	140	150	160	170	180
m919.pep	YFTPQWVAGNGSLAGTVTGYEYEPVLKGD	DRRTAQARFPIYGIPDDFISVPLPAGLRSGKA				
g919	YFTPQWVAGNGSLAGTVTGYEYEPVLKGD	GRRTERARFPIYGIPDDFISVPLPAGLRGGKN				
	130	140	150	160	170	180
m919.pep	LVRIRQGTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQGTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGSLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGSLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
m919.pep	KLGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
g919	KLGTSMQGIKAYMRNPQRLAEVLGQNPSYIFFRELAGSGNEGVPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
g919	IDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	370	380	390	400	410	420
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT  ACCTATTCCG  CGCCGCCCTG  TCGGCATCG  CCGCCGCCAT
51  CCTCGCCGCG  TGCCAAAGCA  AGAGCATCCA  AACCTTTCGG  CAACCCGACA
101 CATCCGTCAAT  CACAGCGCCG  CGAGCGCCGA  TCGGCATCCC  GACCCCGCCG
151 GGAACGACGG  TCGGCGGCGG  CGGGGCCGTT  TATACCGTTG  TGCCGCACCT
201 GTCCCTGCCC  CACTGGGCGG  CTGAGAAATT  CGCCAAAAGC  CTGCAATCCT
251 TCCGCCTCGG  CTGCGCCAAT  CTCGAAAACT  GCCAAGGCTG  GCAGGATGTG
301 TCGGCCCAAG  CCTTTCAAAC  CCCGCTCCAT  TCGGTCAGG  CAAAACAGTT
351 TTTTGAACGC  TATTTACGCG  CGTGGCAGGT  TGCAGGCAAC  GGAAGCCTTG
401 CCGGTACGGT  TACCGGCTAT  TACGAGCCGG  TGCTGAAGGG  CGACGACAGG
451 CGGACGGCAC  AAGCCCGCTT  CCCGATTATC  GGTATTCCCG  ACGATTTTAT
501 CTCGTCGCC  CTGCCTGCGG  GTTTCGGAG  CGGAAAAGCC  TTGTCCGCA
551 TCAGGCAGAC  GGGAAAAAAC  AGCGGCACAA  TCGACAATAC  CGGCGGCACA
601 CATACGCGCG  ACCTCTCCCA  ATTCCCATCT  ACTGCGCGCA  CAAACGGCAAT
651 CAAAGGCAGG  TTTGAAGGAA  GCGCCTTCCT  CCCCTACCAC  ACGCGCAACC
701 AAATCAACGG  CGGCGCGCTT  GACGGCAAAG  CCCCGATACT  CGGTTACGCC
751 GAAGACCCCG  TCGAACTTTT  TTTTATGCAC  ATCCAAGGCT  CGGGCCGTCT
801 GAAAACCCCG  CTGCGGCAAT  ACATCGCAT  CGGCTATGCC  GACAAAAACG
851 AACATCCCTA  CGTTCCATC  GGACGCTATA  TGGCGGACAA  AGGCTACCTC
901 AAGCTCGGG  AGACCTCGAT  GACGGGCATC  AAAGCCATAT  TGAGCAAAAA
951 CCCGCAACGC  CTCGCCGAAG  TTTTGGGGCA  AAACCCAGC  TATATCTTTT
1001 TCCGAGAGCT  TACCGGAAGC  AGCAATGACG  GCCCTGTCCG  CGCACTGGGC
1051 ACGCCGCTGA  TGGCGAGTA  CGCCGGCGCA  GTCGACCGG  ACTACATTAC
1101 CTTGGGCGCG  CCTTATTTTG  TCGCCACCAG  CCATCCGGTT  ACCCGCAAA

```

```

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPQVAVGN GSLAGTVTGY YEPVLKGGDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNP YIFFRELTGS SNGFPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
          10      20      30      40      50      60
m919.pep MKKYLFRALYLGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
          |||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
          70      80      90      100     110     120

          130     140     150     160     170     180
m919.pep YFTPQVAVGNGLAGTVTGYEYEPVLKGGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
          |||
a919      YFTPQVAVGNGLAGTVTGYEYEPVLKGGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
          130     140     150     160     170     180

          190     200     210     220     230     240
m919.pep LVRIRQTGKNSTIDNTGCTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
          |||
a919      LVRIRQTGKNSTIDNTGCTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
          190     200     210     220     230     240

          250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||
a919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          250     260     270     280     290     300

          310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMRQNPQRLAEVLGQNPYSYIFFRELAGSSNDGFPVGALGCTPLMGEYAGA
          |||
a919      KLGQTSMQGIKAYMQQNPQRLAEVLGQNPYSYIFFRELTCSSNDGFPVGALGCTPLMGEYAGA
          310     320     330     340     350     360

          370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

          430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
          |||
a919      QKTTGYVWQLLPNGMKPEYRPX
          430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAACTT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggtt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGCgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaaa gccgAttttc
551 CCGATcaaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEK GK ENMIQRGTYN YQYRSNRPVK DGSYLVTA EY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCOCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTCGCA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKYK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920.pep				PMQLVTEKGKENMIQRGT	YNYQYRSNR	RPVK
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGT	YNYQYRSNR	RPVK			
	40	50	60	70	80	90
g920.pep						
	40	50	60	70	80	90
g920.pep	DGSYLVTAIEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAII					
m920	DGSYLVIAIEYQPTFWSKXKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAII					
	100	110	120	130	140	150
g920.pep						
	100	110	120	130	140	150
g920.pep	KPVGQNLEIVPLDNPADIVHGXRFKVRVLF	FRGEPLPNATVTATFDGFD	TSDRSKTHKTEA			
m920	KPVGQNLEIVPLDNPANIHVGERFKVRVLF	FRGEPLPNATVTATFDGFD	TSDRSKTHXXEA			
	160	170	180	190	200	210
g920.pep						
	160	170	180	190	200	
g920.pep	QAFSDTTDGEGEVDIIP	LRQGFWKASVEYKADFPDQSLCRKQANYTT	LT	TFQIAHSHHX		
m920	QAFSDSTDDKGEVDIIXLRQGFWKANVEHKTD	FPDQSVCKQQANYSTLT	FQIGHSHHX			
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTCGAAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAAACA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCC
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
701	GGAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTGCGA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAH	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDLRHIFS	KPMQLVTEKG	KENMIQRGT	YNYQYRSNR	PVK
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIP	LRQGFWKANVEH	KADFPDQSVK
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

		10	20	30	40	50	60
m920.pep		MKKTLTLLSVSALFATSAHAHRVWVETAH	THGGEY	LKADL	GYGEF	FELEPIAK	DRLHIFS
a920		XKKTLTLLVASALFAASAHHRVWVETAH	THGGEY	LKADL	GYGEF	FELEPIAK	DRLHIFS
		10	20	30	40	50	60
		70	80	90	100	110	120
m920.pep		KPMQLVTEK	GKENMIQ	RGTNYQY	RSNRPVK	DGSYL	VIAEYQPT
a920		KPMQLVTEK	GKENMIQ	RGTNYQY	RSNRPVK	DGSYL	VIAEYQPT
		70	80	90	100	110	120
		130	140	150	160	170	180
m920.pep		MPDASYCEQ	TRMFGK	NI NVNGH	ESADTA	IIITKPV	GQNLEI
a920		MPDASYCEQ	TRMFGK	NI NVNGH	ESADTA	IIITKPV	GQNLEI
		130	140	150	160	170	180
		190	200	210	220	230	240
m920.pep		FRGEPLPN	ATVTAT	FDGFDTS	SDRSKTH	XXEQAQ	AFSDST
a920		FRGEPLPN	ATVTAT	FDGFDTS	SDRSKTH	KTEAQ	AFSDST
		190	200	210	220	230	240
		250	260	269			
m920.pep		KTDFPDQ	SVCQKQ	ANYSTL	TFQIGH	SHHX	
		:					
a920		KADFPDQ	SVCQKQ	ANYSTL	TFQIGH	SHHX	
		:					
		250	260				

q920-1.seq

1	ATGAAGAAAA	CATTGACACT	GCTCGCGcgtt	TcCGCACTAT	TTGCCACATc
51	cgCaCaCCCC	CACCgcGCTT	GGGTCTGAAGC	CgccCACCGa	cAcggCGGGCg
101	AATACCTTTAA	AGCCGACTTG	GTCGTACGGAC	AATTTCACCGa	ACTCGAACCC
151	ATCGcCAAAG	ACCgcCTGCA	CATCTTCAGC	AAACCCGATc	AGCTGGTTFAC
201	CGGAAAGAGT	AAGGAAAAACA	GTATCTCAACG	CGGCACATAC	AACCTACCAAT
251	ACCGACGAGAA	CCGTCCCGTC	AAAGACGGCA	GCTACTCTGT	TACCGCGCAA
301	TATCAGCCTA	CTTTCCGCTC	AAAAAAACAA	GCAGGCTGGA	AACAGGCTGG
351	CATCAAAAGAA	ATGCCGTGAC	CAAGCTATTG	CGAACAAACC	CGTATGTTTCG
401	GTAAAAACAT	TGTCAACGTG	GGACACAGAA	CGCGCGACAC	GGCCATCATC
451	ACCAACACCG	TCCGACAAAA	CTTGGAAATC	GTCCCCGTGC	ACAAATCCCGC
501	CAACATTAC	GTAAGCGCAA	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
551	AACCGCTGCC	ATAGTCCACC	GTTACCGGTA	CATTTGACGG	CTTCGACACC
601	AGCGACCGCA	CGAAACAGCA	CAGAACCGAA	CGCCAGCCT	TCCTCGACAC
651	CACCGACGGC	AAGGCGAAG	TGGAATCATC	CCCTTCTGCG	CAGGCGTTTT
701	GGAAGCGAG	TGTCGAATAC	AAAGCCGATT	TCCCCGATCA	AAGCCTGTGC
751	CAAAAACAGG	CGAATCATAC	AACTTTAAAC	TTCCAAATCG	GCCATTCTCA
801	CACTTAA				

q920-1.pap

1	<u>MKKTLTLLAV</u>	<u>SALFATSAHP</u>	HRVVVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRLHIFS	KPMQLVTEKE	KENMISQRTY	NYQYRSNRPR	KDGSYLVAPE
101	YQPTFRSKNK	AGWQAGKIG	PENDASYCET	RMFGKININV	GHESDATAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDT
201	SOKSATHKTE	AQAFSDT*DG	KGEVDIPLR	QGFWKASVEY	KADFPDQSLC
251	DRQANYTTLT	FOIGHSHH*			

m920-1.seq

1	ATGAAGAAAA	CATTGACACT	GCTCGCGGTT	TCCGCCCTAT	TTGCCACATC
51	CGCCCCACGC	CACCGCGCTC	GGGTCGAAAC	CGGCCACACG	CACCGCGGGC
101	AATACCTTAA	AGGCCGACGT	GGTTCACGGC	AAATTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AGGAAAAACA	TGATTCAACG	CGGCACACAT	AACATACAGT
251	ACCACGAGCA	CCTGCGCGTT	AAGACGGCGA	GTTACCTCGT	CATCGCCGAA

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSVVC
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLIVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLIVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTDDKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFDQSVVCQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCGCCCTAT TTGCCGCATC
51 CGCCACAGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCGGA ACTCGAACC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```
a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

m920-1.pep      10      20      30      40      50      60
m920-1.pep      MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920             XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
m920-1.pep      70      80      90      100     110     120
m920-1.pep      KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKE
a920             KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKQ
m920-1.pep      130     140     150     160     170     180
m920-1.pep      MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNL EIVPLDNPANIHVGERFKVRVL
a920             MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNL EIVPLDNPANIHVGERFKVRVL
m920-1.pep      190     200     210     220     230     240
m920-1.pep      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920             FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
m920-1.pep      250     260     269
m920-1.pep      KTDFFPDQSVQCQKQANYSTLTFQIGHSHHX
a920             KADFPDQSVQCQKQANYSTLTFQIGHSHHX
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```
g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagttctatt tatGtgccca cattgacggA aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```
g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```
m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCC CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCGCCT TGCCCTCTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

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251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPIN' 'TEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCGGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCGCT TGCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGAAAGG GGATTTTCC CAGGCGGAAT
251 GGCAGGATTT TTTTGACAAA GCGGCTTACA AGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgcGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAt acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGT TTTCCAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTGCGCGA CgggcggtAA
801 AATGTTGGTG TCGGCGAcgt tggcgcggg tgcggATGTT CAggcAATCA
851 TTGGCAAAA AACGCCCTG ACGCGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatcc ccggggaac GCTCGAGAT GATGAAAAGg cgGTTTGTt
951 CAACTGGAA ACCGCACCCG GCGTGTtTGA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051 gtcaggGACA TTGCAATTC GCTCGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KKERPAFPA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDfS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRtGNsGR AKFHGARRFY AENRAIDDV AQKYGVPAEL
151 IVAIIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201 EEGGDVFfAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANfYMKQH GWRtGGKMLV SATLAPGADV QAIIGEkTAL TRTVADLKAY
301 GIIPGETLAD DEKAVLfKLE TAPGVFEYfYL GLNNFYTVWQ YNHSRMfVTA
351 VRDIANSfLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAT TCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAACCCG GCGTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAAT ACGGGCAGTT TCCGTGTGCG GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTT TCAAAAAGA ATTGGTCGAG

```

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```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGC GATGTTTTCG CCTTAAAGG
651 CAGCTATGCG GGCAGCAATGG GGATGCCGCA ATTTATGCCT TCAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAC CCGACCGGGC GTGTTTGAAT
1001 ATTATTTGGG CTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1  MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV KGKDFSRAEW QDFFDKAAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APC`DVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEQAAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922 . pep	VSDSGFAANANVRRFVDDEVKGKDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDEVKGKDFSQAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKN TGSFRVADAL					
g922	TGNSGRAKFH GARRFYAENRAVIDDVAQKYGVPaelivaiIGIETNYGKN TGSFRVADAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922 . pep	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922 . pep	DGDGHRDIWGNVGDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922 . pep	ADLKAYGIIPGEELADDEKAVLFLKETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFLKETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
		370				
m922 . pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA  GAAAAATACT  GCCGCTGGCA  ATTTGTTTGG  CGGCTTTGTC
51  TGCCTGTACG  GCGATGGAGG  CACGCCCCGC  CCGGGCAAAT  GAAGCCCAAG
101 CCCCCCGCGC  GGATGAAATG  AAAAAAGAAA  GCCGCCCGCG  GTTTGACGCG
151 GCAGCCGTAT  TTGACGCGGC  AGCCGTACCG  GTATCCGACA  GCGGGTTTGC
201 CGCCAATGCA  AATGTCCGCC  GTTTGTGGA  CGATGAAGTC  GGGAAAGGGG
251 ATTTTCCCG  GCGGAATGG  CAGGATTTT  TTGACAAAGC  GGCTTACAAG
301 GCGGACATCG  TCAAGATTAT  GCACGCCCC  TCCACATCGC  GTCCGTGGTA
351 TGTGTTCCGC  ACGGGAAATT  CGGGCAAGGC  GAAATTTGCG  GCGCGCGGCC
401 GGTTTTATGC  GGAAAACCGC  GCGTTATCG  ATGATGTGGC  GCAAAAATAC
451 GGCGTGCCTG  CCGAACTTAT  CGTGGCGGTT  ATCGGGATTG  AAACGAATTA
501 CGGCAAAAT  ACGGGCAGTT  TCCGTGTGCG  GGACGCATTG  GCGACCTTAG
551 GCTTTGATTA  CCCCCGCCG  GCCGGGTTT  TCCAAAAGA  ATTGGTCGAG
601 CTTTAAAGC  TGGCAAAAGA  AGAAGGCGCG  GATGTTTTCG  CCTTTAAGG
651 CAGCTATGCG  GCGCAATGG  GGATGCCGCA  ATTTATGCCT  TCGAGCTACC
701 GGAAATGGGC  GGTGGATTAT  GACGGGACG  GACATCGGGA  CATATGGGCG
751 AATGTTGGCG  ATGTCGCGGC  ATCGATTGCC  AATTATATGA  AGCAGCACGG
801 TTGGCGCACG  GCGGGGAAA  TACTGGTGT  TGCAACATTG  GCGCCGGGTG
851 CGGATGTCA  GGCAATCATT  GGCGAAAAA  CCGCCCTGAC  GCGGACGGTG
901 GCGGATTGA  AGGCGTACGG  CATCATCCC  GGCGAAGAGC  TTGCCGATGA
951 TGAAAAGGCG  GTTTGTGTC  AACTGGAAAC  CGCACCCGGC  GTGTTTGAAT
1001 ATTATTGGG  CTTGAACAAT  TTTTATACGG  TATGGCAGTA  CAATCACAGT
1051 CGGATGTATG  TAACGGCGGT  CAGGGACATT  GCCAATTCCG  TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA  ICLAALSACT  AMEARPPRAN  EAQAPRADEM  KKESRPAFDA
51  AAVFDAAAVP  VSDSGFAANA  NVRRFVDDEV  GKGDfsraew  QDFFDKAAAYK
101 ADIVKIMHRP  STSRPWYVFR  TGNSGKAKFR  GARRFYAENR  ALIDDVAQKY
151 GVPaelivav  IGIETNYGKN  TGSFRVADAL  ATLGFDYPRR  AGFFQKELVE
201 LLKLAKKEGG  DVFAFKGSYA  GAMGMPQFMP  SSYRKWAVDY  DGDGHRDIWG
251 NVGDVAASIA  NYMKQHGWRT  GGKILVSATL  APGADVQAI  GEKTALTRTV
301 ADLKAYGIIP  GEELADDEKA  VLFKLETAPG  VFEYYLGLNN  FYTVWQYNHS
351 RMYVTAVRDI  ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           190      200      210      220      230      240

           250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKALTTRTV
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRGTGGKILVSATLAPGADVQAIIGEKALTTRTV
           250      260      270      280      290      300

           310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
           310      320      330      340      350      360

           370
m922.pep  ANSLGGPGLX
           ||||||||
a922      ANSLGGPGLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPHLR LLPALFGGWY GAYLGSRMFR HKTAKKRFVY LFRLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGG TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTCGCTT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTGTCCC GCCTGAATTT
451 TTCGTAAAAC TCGGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPHLR LLPALLGGWV GAYFGSMTFK HKTAKKRFVY LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10      20      30      40      50      60
g923.pep  MKRQAFFKPMACAAFLSAVSLRPLVGLGACYAILSLEYAFALYGIDKRRRAVRGKRRIP EHRRL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m923      MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLEYAFALYGIDKRCAIRGQRRIP EHRRL
          10      20      30      40      50      60

      70      80      90      100
g923.pep  LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFR LTVSGNVLATCILID-----
          |||||:||||:||||:| | :|||||:|||||:|||||:|||||:|||||:|||||
m923      LLPALLGGWVGAYFGSMTFKHKTA KKRFFVVLFR LTVSGNVLATLILIIYSGNLNLNQYGVAS
          70      80      90      100      110      120

      110      120
g923.pep  -----YFVPPPELFVKLGQHLX
          |||||:|||||:
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX
          130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCCG
201 CCGTTGGGCG GCGGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAGCG TTTTGTTGTG CTGTTCCGTC TGA CTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGCTGCGG CTTCGTGCGC
451 TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLEYAFAL YGIDKRRRAVR
51  GKRRIP EHRLL LPALFGGWA GAYLGSRIFR HKTAKKRFV VLFRLTVSGNV
101 LATLILIIYS GNLNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

```

      10      20      30      40      50      60
m923.pep  MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLEYAFALYGIDKRCAIRGQRRIP EHRRL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a923      MKRQAFFKLMACAAFLSAVSLRPLVGLGACYAILSLEYAFALYGIDKRRRAVRGKRRIP EHRRL
          10      20      30      40      50      60

      70      80      90      100      110      120
m923.pep  LLPALLGGWVGAYFGSMTFKHKTA KKRFFVVLFR LTVSGNVLATLILIIYSGNLNLNQYGVAS
          |||||:||||:||||:| | :|||||:|||||:|||||:|||||:|||||:|||||
a923      LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFR LTVSGNVLATLILIIYSGNLNLNQYGVAS
          70      80      90      100      110      120

      130      140      150      159
m923.pep  PC-----RTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a923      PXAQRERFSKVLKHQVNRFR TICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          130      140      150      160      170

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
  1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
 51  CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101  AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351  ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAATGCA ACGGCAAACC
501  GACATTGTTG TTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
  1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
 51  KINVFTGKEE SLLSEKDGA LSINTGIGEI PIKL DDGKE LYVERRRYVK
101  TDAAMDKII AHQKKCGQA QAYLDARNAL PSNQTYYQQRQ AAIEQLKRRF
151  EAEFDELEKE IKCNGKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
  1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
 51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TACTTCCTT
      . . . . .
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
  1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAAMDKIIAHQKKCGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
  1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
 51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101  AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151  AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201  AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251  TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301  ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351  ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401  AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451  GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAATGCA ACGGCAAACC
501  GACATTGTTG TTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKOMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKQNYFLH
51  KINVFTGKEE SLLLSEKDG ALSINTGIGE IPIKLSDDGKE ELYVERRRQYV
101 TDAAMKDKEI IAHQKKGQT AQAYLDARNAL PSNQTYYQORQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTGCG TTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTCCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKOMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKQNYFL
51  NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRRQYV
101 KTDAAAMDKI IAHQKKGQT AQAYRDARNA LPSNQTYYQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKOMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKQNYFLNKHVVTKGE					
g925-1	MKOMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKH-KGNYFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRQYVKTDAAMKDKEIAHQKKGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKEIAHQKKGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYYQORQAAIEQLKRRFEAEFDELEKEIKCNK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCGGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRRQYV
51  KTDAAAMDKI IAHQKKGQT AQAYLDARNA LPSNQTYYQH QAAIEQLKRR
101 FEAEFDELEK EIKCNKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKQNYFLNKHVVTKGEESLLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90
				100

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKFCGQTAQAYLDARNALPSNQTYQQH
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKFCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKNGH-PTLLFX
m925-1      LAAIEQLKRRFEAEFDELEKEIKNGRSPALLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCCG
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGCGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCAag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCCG
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGGAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGCGCGCG CCTTACCGCA
401 TCCTGCCCGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAAAC
451 GCGGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCCGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADGGGQVRTL QLNNGNLNI RLVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEESAELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEOYGTWIGQNCROWGASPNVATE

```

1334

```

m926      |||:||||||| |||||:|:| :|
          WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
          130      140      150      160      170      180

a926.seq
1  ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCTGTG GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETQECCAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

```

m926.pep      10      20      30      40      50      60
              MKHTVSASVILLTACAQLPQNNENLWQPS EHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              |||:||||||| |||||:|:| :|
a926           MKHTVSASVILLTACAQLPQNNENLWQPS EHSFTAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

m926.pep      70      80      90      100     110     120
              PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
              |||:||||||| |||||:|:| :|
a926           PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

m926.pep      130     140     150     160     170     180
              WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
              |||:||||||| |||||:|:| :|
a926           WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
              130     140     150     160     170     180

m926.pep      190
              ETETPERCAARTRX
              |||:||||
a926           ETETQECCAAARIQX
              190

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

```

g927.seq
1  atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51  CAGCCCcgca GCcgatTcaa accaTCCGTC CGGACaAaAT GCCCCGCCCA
101 ATACCGAATC cgacGgaaa AACATtaccC TGctcaatgc cTcgtaacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaacATA
201 CCAATCCGAA CACCCCGGCA CATCCGTcAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

```

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```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATA CGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAAGCTCGT CGCATCCATC
601 CTCAAAAACA CACCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

```

g927.pep
  1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAY YGLKANNGNE QEAQKLVASI
201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

```

m927.seq
  1 ATGAAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTC.ACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAAGAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGTAAAA
701 CGAAGCCAAC TACGTCAGCt AAAAAcTGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

```

m927.pep
  1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

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	180	190	200	210	220	230
g927.pep	YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS					
m927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS					
		190	200	210	220	230

	240
g927.pep	AKNX
m927	AKNX
	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1   ATGAAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCPA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAAA  ACAACCCCA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAACCTCG  GGCAACGSAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1   MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGSSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60

	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
a927	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120

	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
a927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

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```

m927.pep      KNX
              |||
a927          KNX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCATATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCACT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAacgctggG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GCGCGCATTA TACATCcgat TATGCagtcg attgCcgga GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat cggtaAATAT TtggcTTtgg
551 tcaattaTCA TTcCaatCCC attcgcgcg ctAtggctat taCTGcaact
601 gCCCCcaaCC CTTAATcgt caacttgatt gccGaaatTt taggcagtag
651 tttccgtCTT TCttgggggg cgTGGGcgtg ggcaatGCc Gttccccggc
701 ttatcgccct TTtcgTTATG CCTTTGATTT TATATTTTTT GTATCCGCTT
751 GAAATTAAG AAACGCCCAA TGCTGttcAA TTGCCAAAG ACCGCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGTTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGCGC CATTGATTAT GATGGCCGCA
1051 TTTTtaAATA AActcggact gattaaatGG TTCTCCGGAG TGTGGCGGA
1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTta TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGCG TGGAAAGTTC
1451 TGGGATATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK POAWTLLAMF VGVIAAIIGK
51  VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMCKY LALVNYHNSP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTA
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSIVIGSIW WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCACT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

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451 GCGGCGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACCGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATP TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTwyT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGG AAAGAAAAAA
1001 GCGCGTGCGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTGCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGCG GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACGCTA TGTTGCGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTI WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng)

from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
g929.pep	AVGLVAVTGVGTADKPGAAMSDALSAFANPLIWLIAIAVMSRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGVGTADKPGAAMSDALSAFANPLIWLIAIAVMSRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g929.pep	LALVNYHNSNPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVPAITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVPAITGN					
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAHYAHYMFASSTTAHITAMFGAFLAAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAHYAHYMFASSTTAHITAMFGAFLAAAVSLNAPAM					
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1   ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGT TGGTCCGAGT
201 AACCGCGCTA ACCGCCGACA AACCGGGTGC GCGCATGAGC GATCGCTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGCTGGGG ATGCGTATCG GATATTGTGT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTGTTATG CTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTGCCCAGG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGTTGTAT TGAATTGGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGGCG ATTTTTCGCT GCTGCGGTTT CACTGAATGC
1251 CCCGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGCTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTATA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTC TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

a929.pep
 1 MKLGFKPIPL AIAAVLCAIV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
 401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIEFFVIGSIW WKVLGYW*

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCAIVLALPVPDGVK	PQAWTLLAMF	IGVIAAIIGK	AMPLGALSII		
a929	MKLGFKPIPLAIAAVLCAIVLALPVPDGVK	PQAWTLLAMF	IGVIAAIIGK	AMPLGALSII		
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV	TADKPGAAMS	DALSAFANPL	IWLIAIAVMIS	SRGLLKTGL	MRIGYLFIAV
a929	AVGLVAVTGV	TADKPGAAMS	DALSAFANPL	IWLIAIAVMIS	SRGLLKTGL	MRIGYLFIAV
	130	140	150	160	170	180
m929.pep	FGRKTLGIGY	SLALSELLLA	PVTSPNTARG	GGIHPIMQS	IAGSYGSNPA	KGTEGKMGKY
a929	FGRKTLGIGY	SLALSELLLA	PVTSPNTARG	GGIHPIMQS	IAGSYGSNPA	KGTEGKMGKY
	190	200	210	220	230	240
m929.pep	LALVNYHSNP	ISSAMFITAT	APNPLIVNLI	AENLGSSFRL	SWGAWAWAMA	VPGVIAFFVM
a929	LALVNYHSNP	ISSAMFITAT	APNPLIVNLI	AENLGSSFRL	SWGAWAWAMA	VPGVIAFFVM
	250	260	270	280	290	300
m929.pep	PLILYXLYPPE	EIKETPNAVQ	FAKDRLREMG	KMSADEIIMA	VIFGILLLLW	ADVPALITGN
a929	PLILYFLYPP	EIKETPNAVQ	FAKDRLREMG	KMSADEIIMA	VIFGILLLLW	ADVPALITGN
	310	320	330	340	350	360
m929.pep	HAFSINATATA	FIGLSLLLL	SGVLTWDDVL	KEKSAWDTII	WFGALIMMAA	FLNKLGLIKW
a929	HAFSINATATA	FIGLSLLLL	SGVLTWDDVL	KEKSAWDTII	WFGALIMMAA	FLNKLGLIKW
	370	380	390	400	410	420
m929.pep	FSGVLAESVG	GGLGVSGTAAG	VILVLAYMYA	HYMFASTTAH	ITAMFGAFFA	AAVSLNAPAM
a929	FSGVLAESVG	GGLGVSGTAAG	VILVLAYMYA	HYMFASTTAH	ITAMFGAFFA	AAVSLNAPAM
	430	440	450	460	470	480
m929.pep	PTALMMAAAS	NIMMTLTHYA	TGTSPVIFGS	GYTTMGEWWK	AGFIMSVVNF	LIEFFVIGSIW
a929	PTALMMAAAS	NIMMTLTHYA	TGTSPVIFGS	GYTTMGEWWK	AGFIMSVVNF	LIEFFVIGSIW
m929.pep	WKVLGYW*					

a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

```
m930.seq
1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT IGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

```
m930.pep
1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWWLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNAL SF GTTTTRILAA
151 PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

```
g930-1.seq (partial)
1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCGTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAAG
201 ACGTATTGCA GCATTCGAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGCGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAACTGTGG ACGAGGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACAC ACAGGTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAAACAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACCTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

```
g930-1.pep (partial)
1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTPJ LAAPDLNSG KLQTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYSVSKLW TRETKSYIDD AELTVQRKKT TGWLAELSHK GYIGRSTADF
301 KLYKHGTGM KDALRAPEEA FEGTSPMKII WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLFW
401 QFKPGHQLYL GADVGHVSGO SAKWLSGQTL AGTAIGIRGO IKLGGNLHYL
```

451 IFTGPAKKP EYFQTKKWVT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAAATTA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGCATCAAAC AATTACGCCG TACATTATTC
951 AGCCCCTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCACCGCG CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAGTT
1151 ACATTGATGA TGCCGAACCTG ACTGTACAAC GGCCTAAAAC TCGGGTGTGG
1201 TTGGCAGAAC TTTCCACAAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGGA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTGAGGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGGCAACC TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGA AAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL
201 LNLRLDLEQGL ENLKRLEPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHKKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQA VSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKS YIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWE WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFG VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEH	ARFQFALKRAL	RETGFQAGK	CLHAGNINQIM	SLAQNALIGR	GYTTTRI
g930-1.pep				GKCLHAGDINQIM	SLAQNALIGR	GYTTTRI
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQ	LTLPISYLR	SIRIDRSNDDQ	THAGRIAAFO	NKFPTRSNDL	LNLRLDLE
g930-1.pep	LAAPQDLNSGKLQ	LTLPISYLR	SIRIDRSNDDQ	THAGRIAAFO	NKFPTRSNDL	LNLRLDLE
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLLENLKRLEPTAE	ADLQIVPVEG	EPNQSDVVVQ	WRQRLPYRV	SVGMDSNGSE	ATGKYQG

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```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPHOSDVVVQWXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

              270      280      290      300      310      320
m930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
g930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

              330      340      350      360      370      380
m930-1.pep  NHNGYRYHQAVSGLSEVDYNGKSYNTDFGFNRLLYRDAKRRTYLSVKLWMRETKSYIDD
              220      230      240      250      260      270
g930-1.pep  NHNGYRYHQAVSGLSEVDYNGKSYNTDFGFNRLLYRDAKRRTYLSVKLWMRETKSYIDD
              220      230      240      250      260      270

              390      400      410      420      430      440
m930-1.pep  AELTVQRKKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALRAPEEAFGEGTSRMKI
              280      290      300      310      320      330
g930-1.pep  AELTVQRKKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALRAPEEAFGEGTSRMKI
              280      290      300      310      320      330

              450      460      470      480      490      500
m930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVVRGFDGEMSLSAER
              340      350      360      370      380      390
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHTVVRGFDGEMSLPAER
              340      350      360      370      380      390

              510      520      530      540      550      560
m930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYE
              400      410      420      430      440      450
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYE
              400      410      420      430      440      450

              570      580      590
m930-1.pep  IFTGRALKKPEFFQSRKWASGFQVGYTF
              460      470
g930-1.pep  IFTGRALKKPEFFQTKKWTGFQVGYSEF
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTGCGCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGCT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKIVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTT  GATGGAACCC GATATGGGCA
101 ATATCCGTGT GGTTTTGGAC GAATCCAAAG CCCCCAAAC  CGTGTCTAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCACAGGCGG TGGATTTCAG GAGGACTTGG
251 CACAAAAGCG AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGACCATT CGGCATGGCG CGGACGACAG CCCCCGATTG
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT  CGCCCGCTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTGCG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
  1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAKASDG AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS GFPINLADXX SLDYKNQSGY YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

q931/m931

		10	20	30	40	50	60
g931.pep		MKPKFKTVLTLALLAVSLPSMAATRVLMETDMGNIRLVLDESKAKTVANFVRYARKGFY					
m931		MKPKFKTVLTLALLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRVARKGFY					
		10	20	30	40	50	60
		70	80	90	100	110	120
g931.pep		DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
		: : : : : : :					
m931		DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
		70	80	90	100	110	120
		130	140	150	160	170	180
g931.pep		QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVVPQPVKIRR					
m931		QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPQPVKIRR					
		130	140	150	160	170	180
g931.pep	VVVGQX						
m931	VVVGQX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAAC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGACA CCCATGTTT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCTAAAG CACCCAAAAC CTTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTACCCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACTAGT TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTTC
351 CGCCACCAGC CAATCTTTTA TCAATCTGCT GGACAATGAT TCGCTCAACT
401 ACAAAAAACG ACAATACGCG TATACCGTTT TCGGCAGGGT CGAAAGCGCG
```

1345

```

451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

```

a931.pep
  1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
  51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

```

m932.seq
  1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
  51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

```

m932.pep
  1 MKYIVSISLA MGLAACSPGG FKNPNWDAAS FWELKNYANP YPGSASAALD
  51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

```

g934.seq
  1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTACCCGC

```

1346

```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA SCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCAGCTCAA TGCCGTCTGA AGGGCTTTCA GACGCGATTT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATTT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQO KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGMN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQQGFEHAQP
151 PKCTTGAGGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS XRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 .CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGTA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GCGTGCTGCA AAGCCTGGTC GCGCGGCGCG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGGCAGGC AACCAAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGACAGCT ACCATCAGTC CGCAGCGCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCGCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCCG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTThT GCATTGTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRAAVYL RPIDRKLAAA KPGRRGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

                                     10      20      30
m934.pep                          RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                     |||:|||
g934      MKKIIASALIATFALTACQDDTQARLERQOKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          10      20      30      40      50      60

          40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVGTGXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
          |||:|||
g934      PAQAQANGNNGQPVGTGKRRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQRAGKQIHTGGQPR
          70      80      90      100     110     120

          100     110     120     130     140     150

```



```

m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934          QPRRPSRACCLPSVRTPQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARCLPPSRYARF
              130      140      150      160      170      180

              160      170      180      190      200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934          RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
              190      200      210      220      230

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGACGCTC GCACAGCATC GCGTTTACCAA GTTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AACACCACTT CCTGCCGAAG CACAGGCCAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGCAGGGCA CGAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCTTGG TCGGCGCGGG
301 GCGAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGA
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGGG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACAGCAGGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CCGAGGCGCA CGGTTAACCC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TCGCGGTTTT CGGCAGAAGG
551 CGTATAATTG GAGGTCGCCA TGCCGTCTGA AGGGCTTTCA GACGGCATTT
601 TTGTATTGTG TAGGACACTT GTTATGTTGC CGTTTGTATT TTAGACGGCA
651 TTTTGTTTCC AAGAGTTTGA TGTGGGATG CCAATTCTGA

```

```
a934.pep
1      MKKIIASALI ATFALAACQD DAQARLEQQQ KQIERALQCC L AQQADDTVYC
51     LTPFAVKDTI FAEAQANCIM GQVTVXTPA AVYLRPIDRK LAAAKPGRE
101    GRRVYRQRAG KQIHTGRQRP QSRRPARACR LPSVRTSQCA HQQGFEHAQP
151    PCKTTGGAGA ALPPDNAPAR QLPPRHARF RQKAVNPACQ CRNLGFGTAF
201    LYLLGTLLCC LIFRRHFVS KSLMSGWGF*
```

```

m934.pep      10      20      30      40      50      60
                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                |||||
a934          MKKIIASALIATFALAACQDDAQAARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                10      20      30      40      50      60

                40      50      60      70      80      90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
                |||||
a934          PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
                70      80      90      100     110     120

                100     110     120     130     140     150
m934.pep      QSRRPAPACSLPSVRTPQCAHQQGFEHAQPCKTTGGAXAALPPDNAPKRLQPPPRYARF
                |||||
a934          QSRRPAPACRLPSVRTSQCAHQQGFEHAQPCKTTGGAGAAALPPDNAPARQLPPPRHARF
                130     140     150     160     170     180

                160     170     180     190     200
m934.pep      RQEAVNPARQCRLLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
                ||:|||||
a934          RQKAVNPACQCRLLKGFQTAFYLLGLTLLCCRLIFRRHFVSKSLMSGWQFX
                190     200     210     220     230

```

g935.sec not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTC
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC CAGTATAAAA
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTG CGAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGCGC AACGTTGTT ATGCGGCTG
1251 GGCGCAGGAG TGGCGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFGSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNNRRLPPY MLAGVGVQVL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

```

          10      20      30      40      50      60
m935.pep  MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV
          |||
a935      MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV
          10      20      30      40      50      60

          70      80      90      100     110     120
m935.pep  DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
          |||
a935      DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP
          70      80      90      100     110     120

          130     140     150     160     170     180
m935.pep  AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF
          |||
a935      AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF
          130     140     150     160     170     180

          190     200     210     220     230     240
m935.pep  RKKTEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
          |||
a935      RKKAEGLTGWRFGSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK
          190     200     210     220     230     240

          250     260     270     280     290     300
m935.pep  LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
          |||
a935      LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS
          250     260     270     280     290     300

```

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAATGT GGGGCGTTT CGGAAAAAAT
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAATGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GGCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAAATC
801 AGCTTATGAT GACGGGTTTC GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCA.CGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTGT CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDPAKK RVNNRRLPPY MLAGVGVQVL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTT TGGAAATST GGGGCGTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPVKRET VGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPVKRET VGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPIAKRRNSEVFVSADWRF					
a935	GRTESNVPIAKRRNSEVFVSADWRF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

```
g936.seq
1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGGCTGCT  TCAGCGCAGT  CGTCGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgcAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACTTGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCAccgT  CGCGGTACAA  AAAGTCATTA  CCCTTACCA  AAACCTACGTC
601 CAACGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

```
g936.pep
1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

```
m936.seq (partial)
1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCGTCGAC  CGCCGAACCA  CCGGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCC...
```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

```
m936.pep (partial)
1  MKPKPHTVRT  LIAAIFSLAL  SGCVSAVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATTEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTA...
```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD	RRTTGAQTDDNVMALRIETT				
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAGVAKSVI	DRRTTGAQTDDNVMALRIETT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQRNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFV	QGQIARSEQAAEGVYNYIT				
g936	ARSYLQRNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFV	QGQIARSEQAAEGVYNYIT				
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNV	TYVMGI LTPEEQAQIT				
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTCCCG	CCGTCTTCA
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGT	CCGGCGGTG
101	GCGCGAAATC	CGCGCTCGAC	CGCCGAACCA	CCGCGCGCA	AAACGAGAT
151	AACGTAATGG	CGCTGCGTAT	CGAAACCAAC	GCCCGCTCT	ATCTGCGCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCGGT	GTGGGTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACTGAAGG	CGAGAAACA
301	TTCTGCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCGCA	CCGTGTACA
351	CTACATTACC	GTGCGCTCCC	TGCCGCGCAC	TGCCGCGGAC	ATCGCGCGC
401	ACACTTGGAA	CACATCCAAA	GTCCGCGCCA	CGCTGTGGG	CATCAGCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACTACGT
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGCGGTACAA	AAAGTCATCA	CCCTCTACCA	AACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880: ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVG	AAVGAASVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQRNNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTVVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD	RRTTGAQTDDNVMALRIETT				
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVAKSAVD	RRTTGAQTDDNVMALRIETT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQRNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFV	QGQIARSEQAAEGVYNYIT				
a936	ARSYLQRNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFV	QGQIARSEQAAEGVYNYIT				
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA  AACACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGGGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcgaACCA  CCGgcgcgca  AACCgATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCAAC  GCCCGTTTCT  ACCTGCCCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAACTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAALAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACCTTGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCAccgT  CGGCGTACAA  AAAGTCATTA  CCCTCTACCA  AAACACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYPQISV  VGYNRHLLL  GQVATEGEKQ
101 FVQGIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGCGCGCA  AACCgACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCAAC  GCCCGTTTCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCCGGCGAC  ATCGCCGGCG
401 ACACCTTGAA  CACATCCAAA  GTCCGCGCCA  CGCTGTTGGG  CATCAGCCCC
451 GCCACACAGG  CGCGCGTCAA  AATCGTTACC  TACGGCAACG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACCGT  CGGCGTACAA  AAAGTCATCA  CCCTCTACCA  AAACACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT  LIAAIFSLAL  SGCVS AVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYPQISV  VGYNRHLLL  GQVATEGEKQ
101 FVQGIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIV  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAAGSAVD RRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLHLGQVATEGEKQFVQGIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLHLGQVATEGEKQFVQGIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVHIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCGA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGGTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGGTGTACA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTTACCA AAACCTACGC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVG AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GOVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTEDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSAVDRRTTGAQTEDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLGQVATEGEKQFVGQIARSEQAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLGQVATEGEKQFVGQIARSEQAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51  CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACCTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTCGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAATAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCTTT TCCCTCACCG
551 CCGCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCCGGC CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCAGCTTTC AACGTTTCAG GGCAAAGCAG TTCCGAAC TG AAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLNSENRA
51 ALASPVIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIY
101 SSGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLDSDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRIIDGKK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAACTT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCCG
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG AC33CAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCTT CCAGAAACAC ATCCACCTAC
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND MLVGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLDSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIOWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVOHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS TYLNSENRAALASPVIYQ
          || || : : : : : : : : : : : : : : : : : : : : : : : : : :
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS TYLNSENNR AELAAPVYIQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
g937.pep  TGSASFIPVPT EIQENGSTNDMLACTLGLRYGLTGNTDIY GSGSYLWHEERKLDGNGKTR

```


[illegible]

a937.seq

```
1 ATGAAGCGCA TCTTTTGGC CGCCTTGCCC GCCATCCTGC GTTATCCGG
51 TTATGCCGAC GTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACTCCAC TGAAACAGCA AAACAACCGC
151 GCGGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAAAACG GACGAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAA CGACATTTAC
301 GGCACGCGCA GCTATCTGTG TCACGAAGAA CGAAACTCG ACGGCAACGG
351 CAAACCCGCA AACAAACGGA TCTCCGAA ATCCCTCGGC ATCAGCCACA
401 CCTTCTCTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGCGGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAGACG CCAATTACTG GATGCTGAAT CCAATATAT CCTTCGCGCG
651 CAACGACAGA ATCAGCTCTCA CGGGCGGCAT CCAATGGGTG GCGAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAACCACGGG CTTTAAACGG
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 CGGTACAGCA TACGTTTTAA
```

```
a937.pep      1 MKRIFLPALP  AILPLSAYAD  LPLTIEDIMT  DKGKWKLETS  LTYLNSENNE
      51 AELAAPVYIQ  TGATSFPIPI  TLOIEGNSNT  DMLVGLTLGL  YGLTGNTDIT
     101 GSGSYLWHEE  RKLDGNGKTR  NKRMSDVSLG  ISHTFLKDDK  NPALISFELS
     151 TVYKESPNKA  SSGKSWLIGA  TTYKALDPVV  LSLTAAYRIN  GSKTLLSNTF
     201 YKAGNYWMLN  PNISFAANDR  ISLTGGIQWL  GKQPDRLDGG  KESAPNTSTY
     251 AHFGAGGFET  KTTALNASAR  FNVSGQSSEE  LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
a937	:					
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSNNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937						
	TGATSFIPIPTEIQENGSNNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVS	LGISHTFLKDDKN	PALISFLESTVY	ERSRNKASSGK	SWLIGATTY	HAIDPIV
a937	NKRMSDVS	LGISHTFLKDDKN	PALISFLESTVY	ERSRNKASSGK	SWLIGATTY	HAIDPIV
	190	200	210	220	230	240
m937.pep	LSLTAAYR	INGSKTLSDG	IRYKSGNYLL	NPNISFAAND	RISLTGGI	QWLGRQPD
a937	LSLTAAYR	INGSKTLSSN	TRYKAGNYW	MLNPNISFA	ANDRISLT	GGIQLWLG
	250	260	270	280	290	
m937.pep	RESSRNT	STYAHFGAG	FGFTKTTAL	NASARFNV	SGQSSSEL	KFGVQHTFX
a937	KESARNT	STYAHFGAG	FGFTKTTAL	NASARFNV	SGQSSSEL	KFGVQHTFX

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLFAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTGCGC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLFAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQOPKSGEA NPKNPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVIEQ MNAYKSGQRK NTIMEDIANR MSEDLLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLFAFV	LAAGAVSASP	KADVEKGQV	AATVCAACHA	ADGNSGIAMY	PRLAAQHTAY
a939	MKRLTLFAFV	LAAGAVSASP	KADVEKGQV	AATVCAACHA	ADGNSGIAMY	PRLAAQHTAY

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNA P
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDILNVSIFYAKQQPKSGEANKPENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAG SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

```

m950/g950      86.6% identity in 112 aa overlap
              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASH ATGVHKSANG SCGASESAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGAAGSKAG					
m950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a950.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKK					
m950	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKK					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACGCTGTTGG CGGCTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG CGCGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CCGGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCGCTCG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCTCGCG TAAGCCGGAT GATGCCATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACFAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCAGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAG ACGACCCGAC GCCCGAAGTT GCCGCCCATT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGACGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GGGCGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAGAAD VELPKVEGKV LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 FEVAERALEM AVSLNAFEQA EMIIYQKWRQI EPIPGEAQKR AGWLRNVLRRE
151 GGNQHLDDGLE EVLAQSDDDVQ KRRIFLLLVQ AAVQQGGVQAO KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL ORLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFEEQTDTON LSAVWQEMEI MNLVSLRKPQ DAYARLNVLI
301 EHNPNANLYI QAAILAANRR EGASVIDGYA EFAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFQKGV LAAAAAAELD GGRAALRQIG
401 RVFKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLRF
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTC AAGAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGGCGCAGG CTTGCGGCAG TGGGCGAGCG
201 GGTAAATCAG ATATTACGT TGCTGGGAGG GGAAACCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCGGA ACGGCGCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTATACA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGGGAAGAA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA SCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCGCTCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTT
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGGGAAGAA CGAAAAGAAG GTGCTTCGCT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTGGAAG CTGCCCCGTA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTGAGTTGT
1401 TTACGATCGG CTTGGCAAGC GGAAAAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTTCG TTGAAAACGA CCCCAGCCCC GAAGTTGCCG CCCATTGGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCCAACCT TCCCGAAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRRFM LTVLTATLIA GQVSAAGGGA GDMKQKEVG KVFRRQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGETA LQKQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIIYQWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQODGL AQKASKAVRR
201 AALKYEHLEP AAVADVFSV QGREKEAIG ALORLAKLDT EILPPTLMTL
251 RLTKYPEI LDGFFEQTDI QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFQK GVLA AAAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIEKPPA
451 GSNTLQAEAL LVQRSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDOAV DVWTQAAHLT GDKKIWRETL
601 KRGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGVFRKQORYSEEEIKNERAP					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
g951	60	70	80	90	100	110
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNHLDGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGEAQKRAGWLRNVLRERGNHLDGLEEVLAQSDDVQKRRIFLL					
m951.pep	190	200	210	220	230	240
	AQAAVQODGLAQKASKAVRRAALKYEHLPAAVADVVSVOGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTONLSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTONLSAVWQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTQESRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLEHNPANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDEKGVLAATAVELDGGRAALRQIGVRKLPQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKVSAPEYLFDEKGVLAATAAELDGGRAALRQIGVRKLPQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQLALSCLPKREALRGLDKIIEKPPAGSNTELQAEALVQRSVYDRLGKRRKMISD					
g951	420	430	440	450	460	470
	SKIQLALSCLPKREALIGLNNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNGLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNGLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPOPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCAG GCGTATGCCG CCGGCGCGGC GGATGCCAAG CCGCCGAAGC
101 AAGTCGGAAG GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAAACGAAC GCGCACGGCT TCGGCGAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GGCGGAAATG ATTTATCAGA AATGGCGGCA GATTGACCTT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCGC AGGGTGTTTT TATTGTTGCG ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCCGCG GCGTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGTTGCGG GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCG CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAAATAT CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTTC GCCGCTGCGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGACACGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGCG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAACCCG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGCG GCGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCGCGCCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGGCGG
1151 CTGTCGAGTT GGACGGCGGC AGGCGCGCTT TCGGCGAGAT CGGCGGGTGG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCGCC TGTGCAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAC CGCCTGCCCG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTAGATCTT TGAAGGGCGG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CTGCTTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTGCTTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCCGCC CATTTGGGCG AAGTGTGTGT
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPEVKGKVF R KQORYSEEEI
51  KNERARLAAY GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYOKWRIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDGLEEV LAQADEGQNR RVFLLLAQAA VQODGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTIELP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWOEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILAANRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSCLPKD REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQYAYQINP DDTAVNDSIG WAYYLRGDAE SALPYLRYSF
551 ENDPEPEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAAG--AADAKPPKEVGKVFRRKQORYSEEEIKNERAR
          ||| || :||:|:|:|:|:|: ||| | | | | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKKEVGKVFRRKQORYSEEEIKNEPAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE

```

1362

```

m951      |||
          LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE
          70      80      90      100      110      120

a951.pep  120      130      140      150      160      170
          QAEMIIYQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGGQNRVFLLL
          |||

m951      130      140      150      160      170      180
          QAEMIIYQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGGQNRVFLLL
          |||

a951.pep  180      190      200      210      220      230
          AQAAVQQDGLAQKASKAVRRRAALRYEHLPEAAVADVVSQGREFEKAIGALQRLAKLDT
          |||

m951      190      200      210      220      230      240
          AQAAVQQDGLAQKASKAVRRRAALKYEHLPEAAVADVVSQGREFEKAIGALQRLAKLDT
          |||

a951.pep  240      250      260      270      280      290
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||

m951      250      260      270      280      290      300
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||

a951.pep  300      310      320      330      340      350
          LLERNPNADLYIQAAIILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||

m951      310      320      330      340      350      360
          LLERNPNADLYIQAAIILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||

a951.pep  360      370      380      390      400      410
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQCGRYFTADNL
          |||

m951      370      380      390      400      410      420
          YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQCGRYFTADNL
          |||

a951.pep  420      430      440      450      460      470
          SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSVVYDRLGFKKHMISD
          |||

m951      430      440      450      460      470      480
          SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQSVVYDRLGFKKHMISD
          |||

a951.pep  480      490      500      510      520      530
          LERAFRLAPDNAQIMNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYYLK
          |||

m951      490      500      510      520      530      540
          LERAFRLAPDNAQIMNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYYLK
          |||

a951.pep  540      550      560      570      580      590
          GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAHLTGDKKIWRETL
          |||

m951      550      560      570      580      590      600
          GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAHLTGDKKIWRETL
          |||

a951.pep  600      610
          KRHGIALPQPSRKPRK
          |||

m951      KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTST
51     TTACGGAAAA ATCAAAATGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101    TTGTAAAGCA GGATTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151    CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201    AAAACTGGGT AAGGAACAGA TGC CGCGCTC GTTTGAGGAT ATGCGGCGCA
251    TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301    CAGCTCGCGC AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351    AGACGACCAT TTTTCGGTAT TGC CGCGAGT GGATGGCAAT ACGGTTTTGC
401    TTGCCGACCC GTCGCCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTT
451    GAGGCTTGGC AAACCCGTGA GGGAAATTG GCAGGCAGAA TTTTGGCGGT
501    CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551    ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAT ATGGTGGCGT

```


1363

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

```
g952.pep (partial)
1  ..LSYRLNAAPM FNDNPVVGK IKLQSWKARR DFNIVKQDLDFSCGAASVAT
51  LLNNFYGQHL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSFG HVSMSRAQFL
151 EAWQTRGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKKWF
201 AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

```
m952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGGGA TTCAATATT
151 GTAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AACCGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTGA GCGGAAGGGC TATTCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTCATG AGCAGGGCGC AGTTTTTGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

```
m952.pep
1  MMKFYVFL ACVVVLSYR LNAAPMENDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRR
101 MPDLGF EANG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFTQH
201 PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

```

              10      20      30      40
g952.pep      LSYRLNAAPMENDNPVVYGIKLQSWKARRDFNIVKQDLDFSCG
              |||
m952           MMKFYVFLACVVVLSYRLNAAPMENDNPVVYGIKVQSWKARRDFNIVKQDLDFSCG
              10      20      30      40      50      60

              50      60      70      80      90      100
g952.pep      AASVATLLNNFYGQKLT EEEVLEKLGKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ
              |||
m952           AASVATLLNNFYGQTLTEEVLKLDKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ
              70      80      90      100      110      120

              110     120     130     140     150     160
g952.pep      LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSFGHVMSRAQFLEAWQTRGNLAGKI
              |||
m952           LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFLDAWQTRGNLAGKI
              130     140     150     160     170     180

              170     180     190     200
g952.pep      LAVVPKKAETISNKLFFTHHPKRQTEFAVGQVKKWRAAYX
              |||
m952           LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE
              190     200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

```
a952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```

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```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGACG AGTTGGAAAG AAAGGCGGGA TTTCATATTT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGSA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRJ
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYL YRKDDHFSVL RIGDGNVTLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

```

a952.pep      10      20      30      40      50      60
MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
|||||

a952.pep      70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEEKGYALSFEQLAQ
|||||
m952          70      80      90     100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEEKGYALSFEQLAQ
|||||

a952.pep     130     140     150     160     170     180
LKIPVIVYLKIRKDDHFSVLRIGDGNVTLLADPSLGHVSM SRAQFXDAWQ TREGNLAGKI
|||||
m952         130     140     150     160     170     180
LKIPVIVYLKIRKDDHFSVLRIGDGNVTLLADPSLGHVSM SRAQFLDAWQ TREGNLAGKI
|||||

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||:|||||
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCGCCACAC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCCTC GCCAACCTGC AAAGCGGTTC GCAACCCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGCGGCG
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGCGGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep
 1 MKKIIFAALA AAAGVTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
 51 GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYDIFR
 101 VSTKFNFNKG KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCQG
 151 DFSTTIDRTK WGV DYL VNA G MTKNVRIDIQ IEAAKQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq
 1 ATGAAAAA AA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
 101 CCATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC ATTGCCAAC TGCAAAGCGG TTCGCAACAC TTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAAATCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA
 351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCGTCAA CTCAAAGCCG
 401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
 451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep
 1 MKKIIFAALA AAAISTASAA TYKVDEYHAN RFAIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI F DAAQYDIFR
 101 FVSTKFNFNKG KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCQ
 151 GDFSTTIDRT KGM DYL VNV GMTKSVRIDI QIEAAKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAAISTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAAGVTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
m953.pep	70	80	90	100	110	120
	RDGKIDITIPVIANLQSGSQHFTDHLKSADIFDAAQYDIFRFSVSTKFNFNKKLVSV DGNL					
g953	RDGKIDITIPVIANLQSGSQPFTHGLKSADIFDAAQYDIFRFSVSTKFNFNKKLVSV DGNL					
	60	70	80	90	100	110
m953.pep	130	140	150	160	170	180
	TMHGKTAPVKLKAEKFNCYQSPMEKTEVCQGDFSTTIDRTKGM DYL VNVGMTKSVRIDI					
g953	TMRGKTAPVKLKAEKFNCYQSPMAETEVCQGDFSTTIDRTKGM DYL VNVGMTKSVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq
 1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
 101 CTATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAAATCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA

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351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GCGGACTTCA GCACCAACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHENT STNVGGFYGI
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNPNK KRLVSVGNL TMHGKTAPVK LKAERFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAAIGTASAATYKVDEYHANARFSIDHENTSTNVGGFYGITGSVEFDQAK					
m953	MKKIIFAALAAAAISTASAATYKVDEYHANARFAIDHENTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	60
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIREVSTKFNFNKRLVSVGNL					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIREVSTKFNFNKRLVSVGNL					
	70	80	90	100	110	120
a953.pep	TMHGKTAPVKLKAERFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
m953	TMHGKTAPVKLKAERFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTAACAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAACACAGC TCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTHGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLQ KESYQNYRKS MQECLKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCTTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacaqtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CqcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaaacc ccaaagtgtc gaatatattt tgaaaaacgg aaatcttttt
901 attgccaat cttcgacggt aaccttgaag acggatggcg taacggcggg
951 tatgcaaaccc tatcatgcgc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSV VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHCLGICYOM AQVYLAKYRD VANDEQKQVD FREESNRIAS DSRDVSFVQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS VDNKGKPKQSV EYILKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCTTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAGG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAAT CTTGACCGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GGCGGGCGGA
1001 TTGTCGCGCA AGAGAAACAG GGAGACAGAC TGCCTGATT TTCTTTGAAC
1051 TTGAAAATT TGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSV VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHCLGICYOM AQVYLAKYRD VANDEQKQVD FRKESNRIAS DSRNSVFYQN
```

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251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAFV	KLARLFRNA				
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNPNAFVAKLARLFRNA					
	70	80	90	100	110	120
g957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAIALRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAIALRLSRLKEKAKWFHVTEQEHGKEV					
	130	140	150	160	170	180
g957.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	190	200	210	220	230	240
g957.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	250	260	270	280	290	300
g957.pep	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSVDNGKKPQSV EY YLKNLNF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EY YLKNLNF					
	310	320	330			
g957.pep	IAQSSTVTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	340	350	360			
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CAC TTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCCA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCCGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCACGGTA	TATTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCG	GAGAGTAACC
701	GGATTGCGTC	GGA CTGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

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951 CTATCATGCG CAACAGACGT GSTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGAT. TCCTTTGAA CTGGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

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This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARIFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

	10	20	30	40	50
a957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE--NPNAFVAKLARLFRNA				
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA				
	10	20	30	40	50
	60	70	80	90	100
a957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYALAVRLSRLKEKAKWFHVTEQEHGEEV				
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYALALIRLSRLKEKAKWFHVTEQEHGKEV				
	70	80	90	100	110
	120	130	140	150	160
a957.pep	WLDYYIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
m957	WLDYHIGEGGLVAVLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
	130	140	150	160	170
	180	190	200	210	220
a957.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS				
m957	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS				
	190	200	210	220	230
	240	250	260	270	280
a957.pep	DSRDSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF				
m957	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFEYYLKNGNLF				
	250	260	270	280	290
	300	310	320	330	340
a957.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR				
m957	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVR				
	310	320	330	340	350
	360	370			
a957.pep	YAEAAARRSGGRRDLSHX				
m957	YAEAAARRSGGRRDLSHX				
	370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCCGGCAG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGGCGGACG

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101 GCGGTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGCACTA ACGAAAGCGG
201 CAGCCCGGAG AGAACCAGAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCGCAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTCTGGGC
451 GAAACCCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAAAGT
501 CCGTATGGA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CGGGGAAAG GCATAGGCGT TGCCAAACAC GCCCCTCTCG
701 TGTTCGGCGG CGTTCCCTT TCTATACGC CTGGGCGGA CTTCGGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCTT GGCATTATCG GCGAACGCGG CGGACGCTT
901 GACGGCAAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGGCACT TTTACGGCGG
1101 CGAAGAAATC GCGGCAACG TCAACCTCAA CCGCCCGGTA TGGCTGGATT
1151 ATGGCGGCGA GCGGCGGGA GCGAGCTGTA ATGCGCGCCT TTCGGTTAG
1201 AAATACCAGA CGCTGGCAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAACGCA GGCAGGCGCG
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCGGCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTACGCAA
1401 CAGCTGGGGC TACGTCGCGC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGGC AAAGCATCCC GCAGCGTCGG GCGGCTTTG
1501 CCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCGCTG TTCTACAAC
1601 ATATTCTGC CAAATCTCAA AACGACCTGC CCAATTTGCA TTCTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACCGCGCCA ACAGCCTTTC CACCGCGCTG CAGAGCGGTA
1751 TTTTGGACGG CGGCACGGG GAGGAGCGTT TCCGCGCGCG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCT ACTGGGTGGC ATTCGCTCCG GCGGCGATAG
1901 CGGGCGGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCGC CCCCAGGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCTGCC GCTACAAC
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCCTAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1 LARLFLSKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASEAQQA
51 SDLTLGSTCL FCSNESGSPE RTEAAVQSG EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVIN TDWADYDQSG DTVTVGDRFA LQQDGTILRG
151 ETLTYNLDQQ TGEAHNVME TEQGGRRLLQ VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQDILTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTRLEGG GVVQTIEPRL FYNYPKASQ NDLPNFDOSSE
551 SSFGYQGLFR ENLYYGNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLLQADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLLQLKDL SSVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTTG
51 CTTCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTGC AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCACTCG GGCACACCG
401 TTACCGCAGG CGACCCGTTT GCCCTCCAA CAGGACGGTAC GCTGATTCGG
451 GGCAGAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCAAGCC GATCGGAAA AAGGCATAGG CGTTGCCAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACGGC GTTCCCTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGCG AGGTACGCTA CCTGCGGCGG GATTATGCGG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACCGT TCAGGCGGGT
1051 GTCGATTTC ACGAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCGT GTATGGCTGG
1151 ATTATGCGCG CAGGCGCGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CCGTCGAGTG GCGTAAAAAC ACCGCGAGGG
1301 CGCAAAATCG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCCG
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCG GACATCAAA GGGATTTACG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACCGCT CAGCGCAGT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGCGACGA
1901 TCGCAGCGCG CTTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCGG AGAACTACGC CGTCGGTGC ACGTACCGT CCGCACAGGG
2001 CAAAGTCTG AACGCGCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGCG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGG
2351 CCGTTCGCGG CTATATCACC GCCCACTCTC TTTCGCCCGG ACGCAACAAA
2401 CGACCCTGA

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This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1 LARLFLSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQQVVRABGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQCDGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLSPYYFN LAPNLDTFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDHSR
451 QDGSRLLVYP DIKWDFNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSR
501 LPIVNIIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSPGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 OKFYFKDDAV MLDGSVGKKP RNRSDWVAFS SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYLSKSGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLG GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALG	LCFGTHCAAAADVA	AETDNPTAGESVRS	VSVEPIQPTSLSLG	STC	
g958	LARLFSLKPLVLALG	FCFGTHCAA-DTVA	AEEADGRVAEGGA	QGAESAQASDLT	LGSTC	
	10	20	30	40	50	
m958.pep	70	80	90	100	110	120
m958.pep	LFC	SNESGSPERTEAA	VQGSGEASIPEDY	TRIVADRM	EGSQSVQVRAE	GNVVVERNTTL
g958	LFC	SNESGSPERTEAA	VQGSGEASVPEDY	TRIVADRM	EGSKVKVRAE	GSVITIERDGA
	60	70	80	90	100	110
m958.pep	130	140	150	160	170	180
m958.pep	NTD	WADYDQSGD	TVTAGDRFALQ	QDGTILIRGET	LTLYNLEQQT	GEAHNV
g958	NTD	WADYDQSGD	TVTVGDRFALQ	QDGTILIRGET	LTLYNLEQQT	GEAHNV
	120	130	140	150	160	170
m958.pep	190	200	210	220	230	240
m958.pep	SVS	RTAEMLGEGHYK	LTETQFN	TCSAGDAGWY	VKAASVEADRE	KGIGVAKHAA
g958	SVS	RTAEMLGEGHYK	LTETQFN	TCSAGDAGWY	VKAASVEADRE	KGIGVAKHAA
	180	190	200	210	220	230
m958.pep	250	260	270	280	290	300
m958.pep	IF	YTPWADFPLDGN	RKSGLLVPS	LSAGSDGVSL	SVPPYFNLAP	NLDATFAPS
g958	IF	YTPWADFPLDGN	RKSGLLVPS	SVSAGSDGV	SVPPYFNLAP	NLDATFAPS
	240	250	260	270	280	290
m958.pep	310	320	330	340	350	360
m958.pep	FDG	QVRYLRPDYAG	OSD	LTWLP	PHDKKSGRNN	RYQAKWQHRH
g958	FDG	QVRYLRPDYAG	OSD	LTWLP	PHDKKSGRNN	RYQAKWQHRH
	300	310	320	330	340	350
m958.pep	370	380	390	400	410	420
m958.pep	YYR	DFYGNKEIAGN	VNLNRRV	WLDYGGRAAG	GS	LNAGLSVLKY
g958	YYR	DFYGNKEIAGN	VNLNRRV	WLDYGGRAAG	GS	LNAGLSVLKY
	360	370	380	390	400	410
m958.pep	430	440	450	460	470	480
m958.pep	PRL	SVWRKNTGRA	QIGVSAQ	FTRF	SHDSRQDGS	RLVVYPDK
g958	PRL	SADWHKNAG	RAQIGVSAQ	FTRF	SHDSRQDGS	RLVVYPDK
	420	430	440	450	460	470
m958.pep	490	500	510	520	530	540
m958.pep	AT	YYS	LNRFGSQ	EARRVSR	TLPIVNI	DSGATFER
g958	AT	YYS	LNRFGSQ	EARRVSR	TLPIVNI	DSGATFER
	480	490	500	510	520	530
m958.pep	550	560	570	580	590	600
m958.pep	QND	LPNFD	SSS	SFGY	QGLFREN	LYYGNDR
g958	QND	LPNFD	SSS	SFGY	QGLFREN	LYYGNDR
	540	550	560	570	580	590
m958.pep	610	620	630	640	650	660
m958.pep	QK	FYFKDDAV	MLDGS	VGKPNR	SRSDW	VAFASGS
g958	QK	FYFKDDAV	MLDGS	VGKPNR	SRSDW	VAFASGS
	600	610	620	630	640	650
m958.pep	670	680	690	700	710	720
m958.pep	SYR	PAQ	GVNLN	ARYKYGR	NEKIYLK	SDGSYFYD
g958	SYR	PAQ	GVNLN	ARYKYGR	NEKIYLK	SDGSYFYD
	660	670	680	690	700	710

1373

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958          EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958          MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACATATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCGCA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACC GAGCCGCGT CCAAGGCAGC GCGGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTTCG
451 GCGGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGATAT GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCGCG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCTC
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCTGCTC GTTCCCTCAC TGTCCGCGCG
801 TTCCGACGGC GTTCCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGC CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG CCGAGTCCGA
951 CCTGACCTGG CTGCCGACG ACAAGAAAAG CCGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACCAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAACCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC CTGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGC GCGGAGTCC TGCAAACCTT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGA CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTACGCG CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTCTG
2351 CCGTCCCGCG CTATATCCCC GCCACTCTC TTTCCGCGCG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1   LARLFSLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTLSLGSLGSL LFCNSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVFM ETEHGGRRLO SVSRTAEMLG EGHYKLTETO
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

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1374

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251 LDGNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLOAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QTFRSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFFAGIG
601 OKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KPAENYAVGA SYRPAQGVVL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAEEKSSGCG WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFS	LKPLVL	ALGFCF	GTHCAA	ADAVAA	EETDNPTAGGSVRSVSEPIQPTSLSLG
m958	LARLFS	LKPLVL	ALGLCF	GTHCAA	ADAVAA	EETDNPTAGESVRSVSE
	10	20	30	40	50	60
a958.pep	70	80	90	100	110	120
	LFC	SNESG	SPERTEA	AVQSGE	ASIPEDY	TRIVADRMEGQSQVQVRAEGNVVVERNRTL
m958	LFC	SNESG	SPERTEA	AVQSGE	ASIPEDY	TRIVADRMEGQSQVQVRAEGNVVVERNRTL
	70	80	90	100	110	120
a958.pep	130	140	150	160	170	180
	NADWADYDQSGD	TVTAGDRF	ALQDDG	TLIRGETL	TYNLEQQTGEAHNV	RMETEHGGRRLQ
m958	NTDWADYDQSGD	TVTAGDRF	ALQDDG	TLIRGETL	TYNLEQQTGEAHNV	MEIEQGGRRRLQ
	130	140	150	160	170	180
a958.pep	190	200	210	220	230	240
	SVSRTA	EMLGEGHY	KLTTETQ	FNTCSAGD	AGWYVKAAS	VEADREKIGIVAKHAAFFVGGVP
m958	SVSRTA	EMLGEGHY	KLTTETQ	FNTCSAGD	AGWYVKAAS	VEADREKIGIVAKHAAFFVGGVP
	190	200	210	220	230	240
a958.pep	250	260	270	280	290	300
	IFYTPWAD	FPLDGNRK	SGLLVPS	LSAGSDG	VLSVPPYY	FNLA
m958	IFYTPWAD	FPLDGNRK	SGLLVPS	LSAGSDG	VLSVPPYY	FNLA
	250	260	270	280	290	300
a958.pep	310	320	330	340	350	360
	FDGQVRYLRP	DYAGQSDLT	WLPHDKK	SGRNNRY	QAKWQHR	HDISDTLOAGVDFNQVSDSG
m958	FDGQVRYLRP	DYAGQSDLT	WLPHDKK	SGRNNRY	QAKWQHR	HDISDTLOAGVDFNQVSDSG
	310	320	330	340	350	360
a958.pep	370	380	390	400	410	420
	YYRDFYGNKE	IAGNVNLNRR	VWLDYGGRA	AGGSLNAG	LSVLKYQ	TLANQSGYKDKPYALM
m958	YYRDFYGNKE	IAGNVNLNRR	VWLDYGGRA	AGGSLNAG	LSVLKYQ	TLANQSGYKDKPYALM
	370	380	390	400	410	420
a958.pep	430	440	450	460	470	480
	PRLSADWRKNT	TGRAQIGVSA	QTFRSHDS	RQDGSRLV	VYPDIKWDFS	NSWGYYVRPKLGLH
m958	PRLSADWRKNT	TGRAQIGVSA	QTFRSHDS	RQDGSRLV	VYPDIKWDFS	NSWGYYVRPKLGLH
	430	440	450	460	470	480
a958.pep	490	500	510	520	530	540
	ATYYSLNRF	SGQEARRV	SRTLPIVNI	DSGMTFER	NTRMFGG	VLQTLLEPRLFYNYIPAKS
m958	ATYYSLNRF	SGQEARRV	SRTLPIVNI	DSGMTFER	NTRMFGG	VLQTLLEPRLFYNYIPAKS

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	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSSSSFGYGQLFRENLYYGNDRI	NTANSL	SAVQSR	ILDGAT	GEERF	FRAGIG
m958	QNDLPNFDSSSSFGYGQLFRENLYYGNDRI	NTANSL	SAVQSR	ILDGAT	GEERF	FRAGIG
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAF	ASSGIGSR	FILDSS	IHYN	QNDHRA	ENYAVGA
m958	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAF	ASSGIGSR	FILDSS	IHYN	QNDHRA	ENYAVGA
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
	SYRPAQGGKVLNARYKYGRNEKIYLS	DGSGYFYDKLS	QDL	LSAQWPL	TENLS	SAVVRYNYGF
m958	SYRPAQGGKVLNARYKYGRNEKIYLS	DGSGYFYDKLS	QDL	LSAQWPL	TENLS	SAVVRYNYGF
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAEYKSSCGCWGAGVYAQR	YVTGENTYK	NAVFFSLQ	LDLSSV	GRNPALF	
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQR	YVTGENTYK	NAVFFSLQ	LDLSSV	GRNPALF	
	730	740	750	760	770	780
a958.pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKRP					
m958	MDVAVPGYIPAHSLSAGRNRKRP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2936: ORF 959.ng>:

g959.pep
 1 MNIKHLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDHIISF
 51 AQAEKAARAR VGGKITDIDL EHDGRPHYD VEIVKNGQFY KVVVDARTGR
 101 VISSRRDD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq
 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
 51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2938: ORF 959>:

m959.pep
 1 MNIKHLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQFY KVVVDARTGR
 101 VISSRRDD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

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      10      20      30      40      50      60
m959.pep MNIKHLLTSAATALISAPALAHHDGHDGDDHGHAHGHNNKQDKIISRAQAEKAAAF
      10      20      30      40      50      60
g959      MNIKHLLTAAATALLGISAPALAHHDGHDGDDHGHAHGHNNKQDKIISRAQAEKAAAF
      10      20      30      40      50      60

      70      80      90     100     109
m959.pep VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100     109
g959      VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100     109

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAAGTCA AACGCCTTCT CTTGACCGCC GCGCAACCG CACTGATGGG
51 CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGCGCGT STCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCCTTG TCGATGCCCG TACCGGCCCG
301 GTGATTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940: ORF 959.a>:

a959.pep

```

1  MNFKRLLTA AATALMGISA PALAHHDGHS DDDHGHAHQ HSKQDKIISF
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
a959.pep MNFKRLLTAAATALMGISA PALAHHDGHS DDDHGHAHQ HSKQDKIISF
      10      20      30      40      50      60
m959      MNIKHLLTSAATALISAPALAHHDGHDGDDHGHAHGHNNKQDKIISRAQAEKAAAF
      10      20      30      40      50      60

      70      80      90     100     109
a959.pep VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100     109
m959      VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX
      70      80      90     100     109

```

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51 TAAGCCCCCC TTGTTTGAAG CTCGCGGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCGGGCG GCTACATTCT CGACATCCCG
151 AAAGGCAATC TGAACCCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTC TGGAAACAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGC CTTAACCAAG
301 GCCCGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGT
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCTT TGCCTCACTC GCTTCTCAGG CTTCGTATC GCTCATCAAC
451 AATAAAGCG ATGTCGGCAA AACCTGAAG GAAGTGGCA GAAGCCGCA
501 GGTAAAAAAT CTGTTGTAG CCGCGGCAAC GGCAGGCGTA TCCAACAAAT

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1377

```

551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TCGGGGCA.. GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGCGCGG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAAAT AGATCTGGAA GTTAAGAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGTGTC ACAACCGCA CAAAACGCGG TAGAAAATAA TGCGGTAAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAA
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AAATTTGAGA
1401 AAAGACAAAC CTTCCGACG AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDVVPKLS APGGYIVDIP
51 KGNLKTIEIK LAKOPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQOGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGTLLK ELGRSRTVKV LVVAAATAGV SNKLGAASSL TWSETPWVNN
201 LNVHLNAGS AALINTAVNG GSKLDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IIVGTENLRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNPFPGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDIFYLDGQ
501 HKNHLEVFDEK NGNFKFVLNM DGSLNQMKTG AAKGRKLNK *

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a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCCTCAAT
301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGTA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGCG CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGCGCTC AATTACGAGT GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKLV LTTAILATFC SGALAAATSDQ DVKKAATVAI VAAVYNGQEI

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```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKH VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNNLGE
151 NITTFAEETK THIVKIDEKL EAVADTVDKH AEAFNDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKVKAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATHKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

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a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCArTTCCA AGACTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATC GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTCAGC GTTGCAAGTC CGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGACTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAT CTCGTTTTGT TCGTGTATAT GACAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAAATGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTAT CATGAACAGC CGGATATTGA
1101 TTTGAAATG GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQRNTV LVLLKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAPPICRKFK NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVYHQNVDDY YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC CTTGCAAGTC CGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACCC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTGGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCCG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAAATATG TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACCTGATG AATTCGCGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948: ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDVDYGE VHFQGRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEK
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPPDYDVE
401 KERKYQEYLS KVVHQNVVDY.

```

m972/a972 99.3% identity in 422 aa overlap

m972.pep	10	20	30	40	50	60
a972	10	20	30	40	50	60
m972.pep	70	80	90	100	110	120
a972	70	80	90	100	110	120
m972.pep	130	140	150	160	170	180
a972	130	140	150	160	170	180
m972.pep	190	200	210	220	230	240
a972	190	200	210	220	230	240
m972.pep	250	260	270	280	290	300
a972	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGKLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPGKLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTGACAGGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGGCG CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCCGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCCT
651 TTTGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCCGTG CCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcacccg CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcccgttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLR
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEEDTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTGACAGGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCCTCCG CCCGCCGTCT
401 TCGTGCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCGGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

```

1381

651 CTTCCGGCAGC GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep
 1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLRLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLV FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFPGTEYGSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq
 1 ATGACGCGC CACAACCGAA AACAAATTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGGC
 201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CTGCGCTCT
 401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCCGGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGATACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GCGGGCCTGG
701 TCATTCAGGA ATTTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGCGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLLE
51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSKEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSKEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRHLTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
51 TGCCTGCGGC GGTGAGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACA CGCAACACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAACC CGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPAA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVTG
151 HTGDFSVSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAGTGTGA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCGCTTAA AACAAACGGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCTCTCG TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTCTCTCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATATCG CAATTATGTG
601 AAAAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATTTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
1   MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVTG
151 YTGDFSVSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQGKDAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPKGKKVSSSEDLKMNKVGVTGYTGDFSVSKLLGNDNPFIARFENVPLIIKE					
g981	ITQVVLVPKGKKVSSSEDLKMNKVGVTGHTGDFSVSKLLGNDNPFIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVSDSAVIANVVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVSDSAVIANVVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCC
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATCACAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTTG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGAAT TCAGCGACCC
351 GTATTTTGAA ATCACCCTAG TCGTCCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCTTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPGK KISSSEDLK MNKVGCVVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m981.pep	ITQVVLVPGKKVSSSEDLKNMNKVGCVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPGKKISSSEDLKNMNKVGCVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m981.pep	LENGGLDSVVSDDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSDDSAVIANVYKNNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
	250	260				
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattccctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAacgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAaaaaCA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTTC AAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCGGTCAA AGCccccggc tTCGgcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtccggcct GTCTTTGGAA AAAGcgactT TGgaagcATT
951 Gggtcaaac aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCCG
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GAGCGGTGGC AGTGATCAA GTCCGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAG ACCCGGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggcctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTTCG CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG DKAAVALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLPLVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYGMIG MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAaaaaCA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

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651	TCCGTTTGTA	TTGTTGTTTCG	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCGTGTTTT	GGAAACAAGTG	GCAAAAGCCA	GCCGTCGCGT	GTGTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTGC	TGAACAACATC
801	CCGAGGCATC	CTGAAAAACCG	TTCGGCTCAA	AGCCCTTGC	TTCCGGCAGC
851	GCCGCAAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTGCGGCT	GTCCTTTGGAA	AAAGCGACCT	TGGACGACCTT
951	GGGTCAAGCC	AAACGCGATC	AAATCGGTAA	AGAAAACACC	ACCATCATCTC
1001	ACGGCTTTTGG	CACGCAGGCC	CAAAATCGAAG	CGCGTGTTGC	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGCGCTGGC	AGTCACTCAA	GTTCGGTCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAG	ACCGCGTGA	AGACGCGCTG
1201	CACGCTACCC	CGCGACCGGT	TGAAGAAAGC	GTGGTTGCAG	CGCGCGCGGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAATCGTCT	TGGCGCGCGT	TGAGTTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGGC	GACCCGACGC	TGGTTGTGAA
1401	CAAAGTATTG	GAAAGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGCGC
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTCGCG	TGCAACACGC	CGCATCTATC	GCCGCGCTTG	TGCTGACCAC
1551	TGATTGCATG	ATCGCTGAAA	TCCCCGAAGA	CAATCCGCGT	GTGCCTGATA
1601	TGGCGCGCAT	GGGTGGTATG	GCCGCGCATGA	TGTAA	

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGGCAAT	GAAGTCCGTC	AAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCCGT	CCGCGTAACC	TTGGGCCCCA
101	AAGGTCGCAA	CGTAGTCGTT	GACCCGCGAT	TCGGCGGCCC	GCACATCACC
151	AAAGACGGCG	TACACGCTCG	CAAGAAGAAC	GAACTGAAAS	ACAAGTTTGA
201	AAATATGGGC	GCGCAATG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGCGACGGCA	CGGTACGACT	ACCCGCCAGT	TACTGGGCGA	ATCCATCGTT
301	GCGGAAGGTA	TGAAATATGT	TACCGCAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	TGAAAGCCG	TCGCCGCTTT	GGTTGACGAA	CTGAAAAACA
401	TCGCAAAACC	TTGCGACACT	TCTAAAGAAA	TCGCCCAAGT	CGGCTCTATT
451	TCGCGCAACT	CCGACGAACA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGTCGCG	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAAGCTTTTG
551	AAAACGAGCT	GGACGTAGTT	GAAGGTATGC	AGTTCGACCG	CGGCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAA	CAATTCGCTG	CTTTGGACCA
651	TCGCTTTGTA	TTGTTTGTTC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCGTGTGTT	GGACAAGATG	GCAAAAGCCA	GCGCTCCGTT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCCA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGCAATC	CTGAAAAACG	TTGCGGTCAA	AGCCCTTGGC	TTCCGGCGAC
851	GCGCGAAAGC	GATGTTTGCA	GACATCGCCA	TCCTGACGGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCCTTTGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCG	CAAACTGAAG	CGCGTGTTCG	CGAATATCCG
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACATGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGCGTGGC	AGTCATCAAA	GTCGGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGG	AGACGCGCGT
1201	CACGCTACCC	CGCGAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	GTCGCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGCGAATG
1301	CCGACCAAGA	GCGAGGCGTA	CAAATCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTCGCCCAAA	TCGTTGCCAA	GCGACGCGCG	GTAACCCAGC	GGTGTTGTGAA
1401	CAAAATGATT	GAGGCCAAG	GCAACTACGG	TTACACAAGT	GGCAGCGCGG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCAT	TGCAACACGC	CGCATCTATC	GCGGCGTTGA	TGCTGACCAC
1551	TGATTTGCAT	ATCGCTGAAA	TCCCAGAAG	CAAACCCGGT	GTGCCTGATA
1601	TGGCGCGCAT	GGTGGTATG	GCGGCGATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

m982.pep MAAKDVFQGNVVRQKMGVNGVILANAVRVTLGPKGRNVVDRAFGGPHITKDGVTVAKEI
::: :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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g982	IASQNLRFDNRFQKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIIVAEAGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIIVAEAGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLDIAILTG
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLDIAILTG
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCCGCAAT GAAGTCCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCAC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGCT ATGAACCCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCCGCTTT GGTGAAGAG CTGAAAAACA

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1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTCG AAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCGGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTAA AGCTCCGGGC TTCGGCGACC
851 CCGCAAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAACCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAACAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AACTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCG TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCCTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCGCG CAAAGTAACC
1501 CGTTCGCGCG TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA GTTAA

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This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

m982/a982 99.3% identity in 544 aa overlap

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90      100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90      100     110     120

          130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
          |||
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFLRGYLSFYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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	250	260	270	280	290	300
m982.pep	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLI IAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA					
a982	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKGNYGNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCTT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgtCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGCGTGA	TTATTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TGCGGCGCAT
1101	TACGCCGGGA	AAAGAAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcc*acgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

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1351 AGgcgcgggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
  51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGS I
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVVQRGQ
 301 LGVITQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
  1 GTGTTCAAAA AATACCAATA CCTCGCTT.G GCAGCACTGT GTGCAGCCTC
  51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCA...TGA GGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
 351 AGCAGATGAC GCGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCTG CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCGGCCA TCGGCGCGCC CTTGCGCTTC GACAACAGCG TGACCGCGG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGCGGGA TTCATGGGCA TTTCTTTCG CATCCCGATT GACGTTGCCA
 851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTGCG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCTTG CCCGGCAGCC
1001 CCGCAGAACG TGCGCGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GCGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCC CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGCGCGGCGC ACGAAATCTT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGAAC ACGCTGTTTA TCGCATTAAA CTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep..
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
  51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVTGMGS I
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVVQRGQ
 301 LGVITQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
g986	VQSEGPAVVNIQAAPAPRTQNGSGNAETSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGI [*] FAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVI IQEVS YGLAQS FGLDKAGG ALIAK ILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVI IQEVS YGLAQS FGLDKASG ALIAK ILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGH L VVVRVSDAAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGKN					
g986	AGITLQTHTDSSGKHL VVVRVSDAAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGC GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAAC TGTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCC CCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AAGCCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTTCGGCTT GACAACAGCG TGACCGCGCG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGCGA TTCATGGGCA TTTCTTCG CATTCCGATT GACGTTGCCA
851 TGAATGTCG CGAACAGCTG AAAAAACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTGGGACAAA GCCGGCGGCG CACTGATTGC CAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCCGGCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAA CCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAG--FGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAFRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDG YILTN THVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO

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1393

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301 LGVIIQEVSY GLAQSFGLK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLLVVVR VSDAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

```

g987.seq
1 ATGAAACAC GCAGCCTCAT TTCCTTTTA TGCTCCTTC TCTGTTTCATG

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1394

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51  TTCTTCATGG TTGCCCCCAC TGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCGC CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGACA TTTCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcggc GTGCGGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtctt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTcGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGcAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGCA
1001 CAGACGCACT GGCAAAACTG GTGcAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGCGGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGACG
1201 TCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGgacg gCAAAACGAT
1251 CTTcATCGGC TCATTCAACC TCGACCCCG TTCCGcACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCGC AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCGGA
1451 ACGAACCcGA AGCCAAACTT TGAaACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51  PHNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LOWHDPATRK TYPNEPEAKL WKRIAAILLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGAAGAAGC GACGGAAAGC CGTCATTTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCGC CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGcAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCACACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTTCGTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCGGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSSSW LPPIEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLO DALKQPEKSV YLVSPYFVPT KSGTDLAKL VQGDIVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPIEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPIEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATLVA					
g987	RKPPIAGRLODALKQPEKSVYLVSPYFVPTKSGTDLAKLVQGDIVTVLTNSLQATLVA					
	310	320	330	340	350	360

1396

```

|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL|TNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLA|TTPAYAYRVTLDRHNRLQWHDPATRK
          |||||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLA|TTPEYAYRVTLDKHNRLQWHDPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTTCATGG TTGCCCCCAC TGGAGAAGAC GACCGAAAGC CGTCATTTC
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGTACCT GACCGACTTC CCCCGCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGCTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTTCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCTT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCGCG GCGGCTGCAA GACGCGTCA AACAGCCGCA
951 AAAAAGCGTC TATCTGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGCGGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAAGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
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1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

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a987.pep
1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNIEV RLENPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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